

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2003, 01:43:10 : Search time 140 Seconds
(without alignments)
197.972 Million cell updates/sec

Title: US-09-988-982-1

Perfect score: 1070

Sequence: 1 MCGNNMSTPLPAIVPAARKA.....CQCEMDVKQFDIKLPPID 208

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1055	98.6	207	AAV09530	Human lysophosphol
2	1037	96.9	219	AAV09530	Human colon cancer
3	1034	96.6	230	AAV09531	Human lysophosphol
4	1034	96.6	230	AAU85132	Human lysophosphol
5	1034	96.6	230	AAU85134	Human lysophosphol
6	1034	96.6	263	AAU85134	Human colon cancer
7	1034	96.6	275	ABG07277	Human colon cancer
8	1028	96.1	230	AAU85133	Human brain lysoph
9	968	90.5	230	AAU85133	Mouse lysophosphol
10	949	88.7	214	AAV69296	A human lysophosph

11	947	88.5	230	AAU85136
12	713	66.6	231	AAU85136
13	490	45.8	216	ABB67341
14	406.5	38.0	119	AAV48392
15	356	33.3	89	ABG07276
16	265	24.8	235	ABB62492
17	244	22.8	218	AAU85134
18	244	22.8	218	AAU85134
19	227.5	21.3	227	AAU85134
20	218	20.4	232	AAU85134
21	218	20.4	232	AAU85134
22	205.5	19.2	255	AAU85134
23	198.5	18.6	233	AAU85134
24	193	18.0	169	AAU85134
25	193	18.0	169	AAU85134
26	193	18.0	169	AAU85134
27	193	18.0	169	AAU85134
28	193	18.0	169	AAU85134
29	193	18.0	169	AAU85134
30	187.5	17.5	223	AAU85134
31	184.5	17.2	169	AAU85134
32	132	12.3	155	AAU85134
33	132	12.3	155	AAU85134
34	128.5	12.0	243	AAU85134
35	118	11.0	60	AAU85134
36	108	10.1	319	AAU85134
37	95.5	8.9	299	AAU85134
38	95	8.9	308	AAU85134
39	93	8.7	584	AAU85134
40	92	8.6	1001	AAU85134
41	90.5	8.5	639	AAU85134
42	90	8.4	308	AAU85134
43	89.5	8.4	219	AAU85134
44	89.5	8.4	219	AAU85134
45	88.5	8.3	252	AAU85134

ALIGNMENTS

RESULT 1	AAV09530	standard; Protein; 207 AA.
XX	AAV09530:	
XX	19-JUL-1999 (first entry)	
XX	Human lysophospholipase NHP.	
XX	Human: lysophospholipase; NHP: cell proliferation; arteriosclerosis;	
XX	atherosclerosis; buritis; cirrhosis; hepatitis; myelofibrosis;	
XX	mixed connective tissue disease; paroxysmal nocturnal haemoglobinuria;	
XX	polycythemia vera; psoriasis; primary thrombocytopenia; cancer;	
XX	inflammation; Addison's disease; AIDS; allergy; asthma; bronchitis;	
XX	immune response; ankylosing spondylitis; autoimmune haemolytic anaemia.	
XX	Homo sapiens.	
XX	Location/Qualifiers	
XX	Key	128
XX	Misc-difference	/label= unknown
XX	FT	/note= "encoded by GNT"
XX	FT	133
XX	Misc-difference	/label= Gly
XX	FT	/note= "encoded by GCK"
XX	MO9849319-A1.	
XX	05-NOV-1998.	
XX	29-APR-1998:	98WO-US08782.

Mouse lysophosphol
Human hydrolyase-1i
Drosophila melanog
Human prostate can
Novel human diagno
Drosophila melanog
Esterase which hyd
Microbial esterase
Human lysophosphol
Plant SDF encoded
Herbicidally activ
Zea mays protein f
Human secreted pro
Human secreted pro
Human secreted pro
Human lysophosphol
Secreted protein #
Human secreted pro
Herbicidally activ
Human MDR1 SFG ID
Plant SDF encoded
Plant SDF encoded
Chlamydia pneumoni
Human 5' ESR seque
Listeria monocytoc
Arabisopsis thaliana
Streptococcus poly
Propionibacterium
Drosophila melanog
Human protein sequ
Group B Streptococ
Mycobacterium tube
Amino acid sequenc
Protein involved 1

Query Match	Best Local Similarity	98.6%	Score 1055;	DB 20;	Length 207;
Matches	206;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	1	MCNNNSITPLAIVPAARAKATAAIVFLHGLGDTGPPRPPTLMMNNVAMPSPWIIIGLSPDS	60		
DB	1	MCNNNSITPLAIVPAARAKATAAIVFLHGLGDTGPPRPPTLMMNNVAMPSPWIIIGLSPDS	60		
QY	61	QEDDSGIRKAQENIKRLIDQEVKNGKIPSNRIILGGFSOGGALSIVALTALTOOKLAGVTAL	120		
DB	61	QEDDSGIRKAQENIKRLIDQEVKNGKIPSNRIILGGFSOGGALSIVALTALTOOKLAGVTAL	120		
QY	121	SFTLLPLRXSFPOGPIGGANRDISILQCHGDCDPLVPLMFSGSLTVEKLTLYNPANVTFT	180		
DB	121	SFTLLPLRXSFPOGPIGGANRDISILQCHGDCDPLVPLMFSGSLTVEKLTLYNPANVTFT	180		
QY	181	YEGMMHSSCOQEMMDYKQFTDKLLPPI	207		
DB	181	YEGMMHSSCOQEMMDYKQFTDKLLPPI	207		
RESULT 2					
AAAG75019					
ID	AAAG75019	standard;	Protein;	219	AA.
XX	AAAG75019;				
XX	03-SEP-2001	(first entry)			
XX	Human colon cancer antigen protein SEQ ID NO:5783.				
XX	Human: colon cancer; colon cancer antigen; diagnosis; detection;				
XX	colorectal carcinoma.				

XX	Homo sapiens.
OS	
XX	MO200122920-A2.
XX	
PD	05-APR-2001.
XX	
PF	28-SEP-2000; 2000WO-US26524.
PR	29-SEP-1999; 99US-0157137.
PR	03-NOV-1999; 99US-0163280.
PA	(HUMA-) HUMAN GENOME SCI INC.
PI	Ruben SM, Barash SC, Birse CE, Rosen CA;
DR	WPI: 2001-235357/24.
DR	N-PSDB; AAH34424.
PT	Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX	useful for preventing, diagnosing and/or treating colorectal cancers -
XX	
PS	Claim 11; Page 7301-7302; 9803pp; English.
XX	
CC	AAH32943 to AAH37195 and AAG37514 to AAG77788 represent human colon
CC	cancer-associated nucleic acid molecules (N) and proteins (P), where
CC	the proteins are collectively known as colon cancer antigens. The colon
CC	cancer antigens have cytostatic activity and can be used in gene
CC	therapy and vaccine production. N and P may be used in the prevention,
CC	diagnosis and treatment of diseases associated with inappropriate P
CC	expression. For example, N and P may be used to treat disorders
CC	associated with decreased expression by rectifying mutations or deletions
CC	in a patient's genome that affect the activity of P by expressing
CC	inactive proteins or to supplement the patients own production of P.
CC	Additionally, N may be used to produce the colon cancer-associated PS,
CC	by inserting the nucleic acids into a host cell and culturing the cell
CC	to express the proteins. N and P can be used in the prevention, diagnosis
CC	and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC	and AAB7789 represent sequences used in the exemplification of the
CC	present invention.
CC	N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC	missing at time of publication, meaning no sequences are present for
CC	SEQ ID NO:1027 to 1052, 7921 and 7922.
XX	
SQ	Sequence 219 AA:
	Query Match 96.9%; Score 1037; DB 22; Length 219;
	Best Local Similarity 97.6%; Pred. No. Be-111;
	Matches 203; Conservative 0; Mismatches 5; Indels 0; Gaps 0
QY	1 MCGNNNSTPLPALVPARAKATAAVIFLHGIGDGTGPRPYTLNANNVAMPMSFIDILGPSDS 60
Db	12 MCGNNNSTPLPALVPARAKATAAVIFLHGIGDGTGPRPYTLNANNVAMPMSFIDILGPSDS 71
QY	61 QEDESGIKOAENIKALIDQEVKNGLIPSNRIILGGFSOGALSLYTALTTOQLAQTAL 120
Db	72 QEDESGIKOAENIKALIDQEVKNGLIPSNRIILGGFSOGALSLYTALTTOQLAQTAL 131
QY	121 SFLLPLRXSPPOEPIGANDDISIIOCHGCDPLVLPMFGSLTVKRLKTLVNPNANTFTFK 180
Db	132 SCWLPLRASTPOEPICGANNDISIIIOCHGCDPLVLPMFGSLTVKRLKTLVNPNANTFTFK 191
QY	181 YEGMHSSCOEQEMDVYKQITDKLLPID 208
Db	192 YEGMHSSCOEQEMDVYKQITDKLLPID 219
RESULT 3	
AAAY09531	
ID	AAAY09531 standard; Protein; 230 AA.
AC	AAAY09531;
XX	

DT 19-JUL-1999 (first entry)
 XX
 DE Human lysophospholipase extended NHLP.
 XX
 KW Human; lysophospholipase; NHLP; cell proliferation; arteriosclerosis;
 KW atherosclerosis; bursitis; cirrhosis; hepatitis; myelofibrosis;
 KW mixed connective tissue disease; paroxysmal nocturnal haemoglobinuria;
 KW polycythaemia vera; psoriasis; primary thrombocytopenia; cancer;
 KW inflammation; Addison's disease; AIDS; allergy; asthma; bronchitis;
 KW immune response; ankylosing spondylitis; autoimmune haemolytic anaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO9849319-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 29-APR-1998; 98WO-US08782.
 XX
 PR 12-FEB-1998; 98US-0022940.
 XX
 PR 29-APR-1997; 97US-0844120.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Hillman JL, Murry LE, Shah P;
 XX
 DR WPI: 1999-326512/27.
 DR N-PSDB; AAX56267.
 XX
 PT New human lysophospholipase (NHLP) polypeptides and polynucleotides
 PT which identify and encode NHLP
 XX
 PS Claim 1; Fig 2; 66pp; English.
 XX
 CC The present sequence is human lysophospholipase (NHLP). The present
 CC invention also describes a method for treating or preventing a disorder
 CC of cell proliferation (e.g. arteriosclerosis, atherosclerosis, bursitis,
 CC cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis,
 CC paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis,
 CC primary thrombocytopenia, and cancers); inflammation (e.g. Addison's
 CC disease, AIDS, allergies, asthma, atherosclerosis, bronchitis) and a
 CC disorder of the immune response (e.g. AIDS, allergies, ankylosing
 CC spondylitis, autoimmune haemolytic anaemia) by administering an
 CC antagonist to NHLP. NHLP proteins, antagonists, antibodies, agonists,
 CC complementary sequences or vectors may be administered in combination
 CC with other therapeutic agents. Antibodies which specifically bind to
 CC NHLP may be used for the diagnosis of disorders characterized by
 CC expression of NHLP or in assays to monitor patients being treated with
 CC NHLP or agonists. The polynucleotides (PNS) encoding NHLP or fragments
 CC may be used therapeutically. In one aspect, the complement of the
 CC polynucleotides may be used where it would be desirable to block the
 CC transcription of the mRNA. Complementary molecules may be used to
 CC modulate NHLP activity or to achieve regulation of gene activity.
 CC Diagnostically, the PNS may be used to detect and quantitate gene
 CC expression in biopsied tissues in which expression of NHLP may be
 CC correlated with disease.
 CC
 XX
 SQ Sequence 230 AA;
 Query Match 96.6%; Score 1034; DB 20; Length 230;
 Best Local Similarity 89.1%; Pred. No. 1.9e-110;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;
 QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTG-----PVRP 38
 Db 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60
 QY 39 VTLMNNVAMPMSWDITIGLSPDSOEDSGIKQAENIKALIDQEVKNKGPSNRITIGGFSQ 98
 Db 61 VTLMNNVAMPMSWDITIGLSPDSOEDSGIKQAENIKALIDQEVKNKGPSNRITIGGFSQ 120
 QY 99 GGAISLYTALTTOOKLAGVTAFLPLRXSFPOGPIGAGNRDISIIQCHGDCDPLVPLM 158
 ||||||||||||||||||| ||| |||||||||||||||||||

Db 121 GGAISLYTALTTOOKLAGVTAFLPLRXSFPOGPIGAGNRDISIIQCHGDCDPLVPLM 180
 QY 159 FGSILTVEXKTLVNPANVTFTYEGAMHSSCOQEMDVKQFIDKLLPPID 208
 Db 181 FGSILTVEXKTLVNPANVTFTYEGAMHSSCOQEMDVKQFIDKLLPPID 230
 RESULT 4
 ID AA085132
 ID AA085132 standard; Protein; 230 AA.
 XX
 AC AA085132;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human lysophospholipase I #1.
 XX
 KW Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antihypertensive; cardiac; lysophospholipase I; inflammation; ischaemia;
 KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antisense gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200210185-A1.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-US22975.
 XX
 PR 31-JUL-2000; 2000US-0629645.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Wyatt JR;
 XX
 DR WPI: 2002-188720/24.
 DR N-PSDB; ABR37030.
 XX
 PT Novel antisense compound useful for treating inflammation,
 PT hyperlipidaemia, and cardiovascular disorders such as atherosclerosis
 PT and myocardial ischaemia, inhibits lysophospholipase I -
 XX
 PS Disclosure; Page 88-89; 131pp; English.
 XX
 CC The invention relates to an antisense compound (I) 8-30 nucleobases in
 CC length targeted to a nucleic acid molecule encoding lysophospholipase I
 CC (II), where (I) specifically hybridizes with and inhibits the expression
 CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
 CC and cardiovascular disorders such as atherosclerosis and myocardial
 CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway. (I) is useful in antisense gene therapy. AA085132-AA085136
 CC represent lysophospholipase I amino acid sequences of the invention.
 CC
 XX
 SQ Sequence 230 AA;
 Query Match 96.6%; Score 1034; DB 23; Length 230;
 Best Local Similarity 89.1%; Pred. No. 1.9e-110;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;
 QY 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTG-----PVRP 38
 Db 1 MCGNNMSTPLPAIVPAARKATAAVIFLHGLGDTGHWAEAFAGIRSSHIIKYICPHAPVRP 60
 QY 39 VTLMNNVAMPMSWDITIGLSPDSOEDSGIKQAENIKALIDQEVKNKGPSNRITIGGFSQ 98
 Db 61 VTLMNNVAMPMSWDITIGLSPDSOEDSGIKQAENIKALIDQEVKNKGPSNRITIGGFSQ 120
 QY 99 GGAISLYTALTTOOKLAGVTAFLPLRXSFPOGPIGAGNRDISIIQCHGDCDPLVPLM 158
 ||||||||||||||||||| ||| |||||||||||||||||||

Db 121 GGALSLVLTALTTOOKLAGVTALSCWLPRLASFPOGPIGGANDRDISILQCHGDCDPLVPLM 180

QY 159 FGSILVEKLTLYNPANVTEFKTEYEGMMSSCOQEMMDVKQFIDKLLPID 208
 |||||
 Db 181 FGSILVEKLTLYNPANVTEFKTEYEGMMSSCOQEMMDVKQFIDKLLPID 230

RESULT 5

AA085134
 ID AA085134 standard; Protein; 230 AA.

AC AA085134;
 XX

DT 08-MAY-2002 (first entry)
 XX

DE Human lysophospholipase I #2.
 XX

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antilipemic; cardiant; lysophospholipase I; inflammation; ischaemia;
 KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antisenese gene therapy.

KW Homo sapiens.
 OS

XX WO200210185-A1.
 PN

XX 07-FEB-2002.
 PD

XX 20-JUL-2001; 2001WO-US22975.
 PF

XX 31-JUL-2000; 2000US-0629645.
 PR

XX (ISIS-) ISIS PHARM INC.
 PA

XX Bennett CF, Wyatt JR.
 PI

XX WPI; 2002-188720/24.
 DR

XX N-PSDB; ABK37045.
 DR

XX Novel antisenese compound useful for treating inflammation,
 PT hyperlipidaemia, and cardiovascular disorders such as atherosclerosis
 PT and myocardial ischaemia, inhibits lysophospholipase I -

XX Disclosure; Page 94-95; 131pp; English.

XX The invention relates to an antisenese compound (I) 8-30 nucleobases in
 CC length targeted to a nucleic acid molecule encoding lysophospholipase I
 CC (II), where (I) specifically hybridises with and inhibits the expression
 CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
 CC and cardiovascular disorders such as atherosclerosis and myocardial
 CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway. (I) is useful in antisenese gene therapy. AA085132-AA085136
 CC represent lysophospholipase I amino acid sequences of the invention.

XX Sequence 230 AA:
 SQ

Query Match 96.6%; Score 1034; DB 23; Length 230;
 Best Local Similarity 89.1%; Pred. No. 1.9e-110;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPARKKATAAIVFLHGLGDTG-----PVRP 38
 |||||
 Db 1 MCGNNMSTPLPAIVPARKKATAAIVFLHGLGDTG-----PVRP 60
 |||||

QY 39 VTLNMYNAMPSPWDIIIGLSPDSQDESGIKQAANKIKALIDQEVKNIGPSNRITILGFSQ 98
 |||||
 Db 61 VTLNMYNAMPSPWDIIIGLSPDSQDESGIKQAANKIKALIDQEVKNIGPSNRITILGFSQ 120
 |||||

QY 99 GGALSLVLTALTTOOKLAGVTALSCWLPRLASFPOGPIGGANDRDISILQCHGDCDPLVPLM 158
 |||||

Db 121 GGALSLVLTALTTOOKLAGVTALSCWLPRLASFPOGPIGGANDRDISILQCHGDCDPLVPLM 180

QY 159 FGSILVEKLTLYNPANVTEFKTEYEGMMSSCOQEMMDVKQFIDKLLPID 208
 |||||
 Db 181 FGSILVEKLTLYNPANVTEFKTEYEGMMSSCOQEMMDVKQFIDKLLPID 230

RESULT 6

AAB53451
 ID AAB53451 standard; Protein; 263 AA.

AC AAB53451;
 XX

DT 09-MAR-2001 (first entry)
 XX

DE Human colon cancer antigen protein sequence SRQ ID NO:991.
 XX

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.

KW Homo sapiens.
 OS

XX WO200055351-A1.
 PN

XX 21-SEP-2000.
 PD

XX 08-MAR-2000; 2000WO-US05883.
 PF

XX 12-MAR-1999; 99US-0124270.
 PR

XX (HUMA-) HUMAN GENOME SCI INC.
 PA

XX Rosen CA, Ruben SM;
 PI

XX WPI; 2000-587534/55.
 DR

XX N-PSDB; AAC98208.
 DR

XX Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer -

XX Claim 11; Page 1568-1569; 2104pp; English.

XX AAG97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnary, nephrotropic, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAB54007 represent sequences used in the exemplification of the present
 CC invention.

XX Sequence 263 AA:
 SQ

Query Match 96.6%; Score 1034; DB 21; Length 263;
 Best Local Similarity 89.1%; Pred. No. 2.3e-110;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPARKKATAAIVFLHGLGDTG-----PVRP 38
 |||||

Db 34 MCGNNMSTPLPAIPAPARKATAAVIFLHGLDGTGHGMAEAFAGIRSSHIIKICPHAPVR 93
 QY 39 VTLMNNVAMPSPWFIDIGLSPDSODESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 98
 Db 94 VTLMNNVAMPSPWFIDIGLSPDSODESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 153
 QY 99 GGALSLYTALTTOOKLAGVYALSFLLPLRXSPGPIGAGNRDISIIQCHGDCDPLVPLM 158
 Db 154 GGALSLYTALTTOOKLAGVYALSFLLPLRXSPGPIGAGNRDISIIQCHGDCDPLVPLM 213
 QY 159 FGSLLTVEKLTIVNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 208
 Db 214 FGSLLTVEKLTIVNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 263

RESULT 7
 ABG07277
 ID ABG07277 standard; Protein: 275 AA.
 AC ABG07277;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #7268.
 XX
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN MO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-0508631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSEQ-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB: AAS71464.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 37636; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 275 AA:
 Query Match 96.6%; Score 1034; DB 22; Length 275;
 Best Local Similarity 89.1%; Pred. No. 2.5e-110;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIPAPARKATAAVIFLHGLDGTGHGMAEAFAGIRSSHIIKICPHAPVR 38
 Db 46 MCGNNMSTPLPAIPAPARKATAAVIFLHGLDGTGHGMAEAFAGIRSSHIIKICPHAPVR 105
 QY 39 VTLMNNVAMPSPWFIDIGLSPDSODESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 98
 Db 106 VTLMNNVAMPSPWFIDIGLSPDSODESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 165
 QY 99 GGALSLYTALTTOOKLAGVYALSFLLPLRXSPGPIGAGNRDISIIQCHGDCDPLVPLM 158
 Db 166 GGALSLYTALTTOOKLAGVYALSFLLPLRXSPGPIGAGNRDISIIQCHGDCDPLVPLM 225
 QY 159 FGSLLTVEKLTIVNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 208
 Db 226 FGSLLTVEKLTIVNPANVTFTKTEGMMHSSCOQEMMDVKQFIDKLLPPID 275

RESULT 8
 AAB82669
 ID AAB82669 standard; Protein: 230 AA.
 AC AAB82669;
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE Human brain lysophospholipase.
 XX
 KW Lysophospholipase; human; brain; lysophospholipid; atherosclerosis;
 KW hypellipidemia; dysrhythmia; myocardial ischaemia; demyelination;
 KW vasotropic; antiatherosclerotic; antilipemic; neuroprotective;
 KW therapy; LysopLA.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Active-site 119
 FT Active-site 174
 FT Active-site 208
 XX
 PN MO200155166-A1.
 PD 02-AUG-2001.
 XX
 PF 28-JAN-2000; 2000WO-0502319.
 XX
 PR 28-JAN-2000; 2000US-0493601.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Dennis EA, Wang A;
 XX
 DR WPI: 2001-483215/52.
 DR N-PSDB: AAH26336.
 XX
 PT Novel recombinant lysophospholipid-specific human brain
 PT lysophospholipase enzyme useful for treating disease states having
 PT elevated concentrations of lysophospholipids, such as atherosclerosis,
 PT hyperlipidaemia -
 XX
 PS Claim 4; Fig 1; 38pp; English.
 XX
 CC The present sequence is that of human brain lysophospholipid-specific
 CC lysophospholipase (LysopLA), a novel member of the K/L hydrolase
 CC family having a catalytic site composed of Ser-119, Asp-174 and
 CC His-208. LysopLAs are critical enzymes that act on biological

CC membranes to regulate the multifunctional lysophospholipids;
 CC increased levels of lysophospholipids are associated with a host of
 CC diseases. The enzyme is widely distributed in almost all tissues,
 CC although levels vary. Lysopla cDNA (see AAH26336) was obtained by
 CC PCR amplification of human brain cDNA using primers (see AAH26337-38)
 CC based on human sequences identified by database screening using a
 CC mouse sequence. The PCR product was expressed in *Escherichia coli*
 CC BL21 (DE3) cells using vector PET28a(a). The recombinant lysopla
 CC protein, which included an N-terminal 6His tag and thrombin cleavage
 CC site, was recovered on an Ni-NTA column. Kinetic analysis showed
 CC that human lysopla displays apparent co-operativity and surface
 CC dilution kinetics. The recombinant lysopla can be used in the
 CC treatment of disease states having elevated concentrations of
 CC lysophospholipids, such as atherosclerosis, hyperlipidaemia, lethal
 CC dysthyrmyia in myocardial ischaemia and segmental demyelination of
 CC peripheral nerves. The lysopla may be supplied for the
 CC enzyme-deficient patient by infusion or by gene therapy (both
 CC claimed). Also claimed is a method of inhibiting human brain
 CC lysopla activity using methyl arachidonyl fluorophosphates.

SO Sequence 230 AA;

Query Match 96.1%; Score 1028; DB 22; Length 230;
 Best Local Similarity 88.7%; Pred. No. 9,4e-110;
 Matches 204; Conservative 0; Mismatches 4; Indels 22; Gaps 1;

OY 1 MCGNNMSTPLPAVPAARKATAVIFLHGLGDTG-----PVRP 38
 |||||
 DB 1 MCGNNMSTPLPAVPAARKATAVIFLHGLGDTGHWMAEAFAGINSHTKTCYCPHAPVVP 60
 OY 39 VTLNNMVAWPSWFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNIGPSNRITLLGGFSQ 98
 |||||
 DB 61 VTLNNMVAWPSWFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNIGPSNRITLLGGFSQ 120
 OY 99 GGLSLYTAITTOOKLAGVTALSFLLPLRXSPFGPGIGANDRISITLQCHGDCDPLVPLM 158
 |||||
 DB 121 GGLSLYTAITTOOKLAGVTALSCWPLRASFSGPINSANRDISITLQCHGDCDPLVPLM 180
 OY 159 FGSILVEKLTIVNPANVTFTKEGMMHSSCOQEMMDVKQFIDKLPPID 208
 |||||
 DB 181 FGSILVEKLTIVNPANVTFTKEGMMHSSCOQEMMDVKQFIDKLPPID 230

RESULT 9
 AAU85133
 ID AAU85133 standard; Protein; 230 AA.

XX AC AAU85133;
 XX DT 08-MAY-2002 (first entry)
 XX DE Mouse lysophospholipase I #1.
 XX
 XX OS Mus musculus.
 XX PN WO200210185-A1.
 XX PD 07-FEB-2002.
 XX PF 20-JUL-2001; 2001WO-US22975.
 XX PR 31-JUL-2000; 2000US-0629645.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Bennett CF, Wyatt JR;
 XX DR WPI; 2002-188720/24.

DR N-PSDB; ABK37037.
 XX Novel antisense compound useful for treating inflammation,
 PT hyperlipidaemia, and cardiovascular disorders such as atherosclerosis
 PT and myocardial ischaemia, inhibits lysophospholipase I -
 XX
 PS Disclosure; Page 92-93; 131pp; English.

CC The invention relates to an antisense compound (I) 8-30 nucleobases in
 CC length targeted to a nucleic acid molecule encoding lysophospholipase I
 CC (II), where (I) specifically hybridises with and inhibits the expression
 CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
 CC and cardiovascular disorders such as atherosclerosis and myocardial
 CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway. (I) is useful in antisense gene therapy. AAU85132-AAU85136
 CC represent lysophospholipase I amino acid sequences of the invention.

SO Sequence 230 AA;

Query Match 90.5%; Score 968; DB 23; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.6e-103;
 Matches 188; Conservative 8; Mismatches 12; Indels 22; Gaps 1;

OY 1 MCGNNMSTPLPAVPAARKATAVIFLHGLGDTG-----PVRP 38
 |||||
 DB 1 MCGNNMVAWPSWFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNIGPSNRITLLGGFSQ 98
 |||||
 DB 61 VTLNNMVAWPSWFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNIGPSNRITLLGGFSQ 120
 OY 99 GGLSLYTAITTOOKLAGVTALSFLLPLRXSPFGPGIGANDRISITLQCHGDCDPLVPLM 158
 |||||
 DB 121 GGLSLYTAITTOOKLAGVTALSCWPLRASFSGPINSANRDISITLQCHGDCDPLVPLM 180
 OY 159 FGSILVEKLTIVNPANVTFTKEGMMHSSCOQEMMDVKQFIDKLPPID 208
 |||||
 DB 181 FGSILVEKLTIVNPANVTFTKEGMMHSSCOQEMMDVKQFIDKLPPID 230

RESULT 10
 AAY69296
 ID AAY69296 standard; Protein; 214 AA.

XX AC AAY69296;
 XX DT 19-JUN-2000 (first entry)
 XX DE A human lysophospholipase protein designated CBPBLH05.
 XX
 XX OS Homo sapiens.
 XX PN WO200009556-A1.
 XX PD 24-FEB-2000.
 XX PF 11-AUG-1998; 98WO-CN00164.
 XX PR 11-AUG-1998; 98WO-CN00164.
 XX PA (UTSH-) UNIV SHANGHAI SECOND MEDICAL.
 XX PI Zhou J, Mao M, Ye M, Zhang Q;
 XX DR WPI; 2000-224281/19.
 XX DR N-PSDB; AAZ61501.

PT New human lysophospholipase gene (designated CBFBLH05) polypeptides and
 PT polynucleotides used to identify agonists, antagonists and inhibitors
 PT for use in (gene) therapy

PS Claim 2; Page 23; 36pp; English.

CC The present sequence represents a human lysophospholipase protein
 CC (designated CBFBLH05). CBFBLH05 polypeptides may be used for
 CC identifying agonists and antagonists/inhibitors, and for detecting
 CC and treating diseases associated with inappropriate CBFBLH05 activity
 CC or levels. CBFBLH05 polypeptides and polynucleotides, agonists,
 CC antagonists and antibodies are used for the treatment of liver diseases,
 CC cancer, autoimmune diseases, and kidney disorders. The polynucleotide
 CC is also useful as a source of primers and probes, and also for detecting
 CC the above diseases. The polypeptide may also be used as a vaccine.

XX Sequence 214 AA:

Query Match 88.7%; Score 949; DB 21; Length 214;

Best Local Similarity 88.4%; Pred. No. 1,le-100;

Matches 191; Conservative 4; Mismatches 11; Indels 10; Gaps 2;

QY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTG-----PVRPVTLNMMNVPMSWD 52
 DB 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTGHWAEAFAGIR--SSHIKYICPHAFD 58
 QY 53 IIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGALSILYALTQQ 112
 DB 59 IIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQGALSILYALTQQ 118
 QY 113 KLAGYATLSFLPLRXSPQGPFGANRDISILQCHGCDPLVPLMFSLTVEKLTIVN 172
 DB 119 KLAGYATLSFLPLRXSPQGPFGANRDISILQCHGCDPLVPLMFSLTVEKLTIVN 178
 QY 173 PANVTFKTYEGMMHSSCOQEMMDVKQFTDKLLPID 208
 DB 179 PANVTFKTYEGMMHSSCOQEMMDVKQFTDKLLPID 214

RESULT 11

AAU85136
 ID AAU85136 standard; Protein; 230 AA.

XX AC AAU85136;

DT 08-MAY-2002 (first entry)

DE Mouse lysophospholipase I #3.

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antiinflammatory; cardiant; lysophospholipase I; inflammation; ischaemia;
 KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antisense gene therapy.

XX Mus musculus.

XX WO200210185-A1.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-US22975.

XX 31-JUL-2000; 2000US-0629645.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Wyatt JR;

XX WPI; 2002-188720/24.

DR N-PSDB; ABK37048.

PT Novel antisense compound useful for treating inflammation,
 PT hyperlipidaemia, and cardiovascular disorders such as atherosclerosis

PT and myocardial ischaemia, inhibits lysophospholipase I -
 XX Disclosure; Page 98-99; 131pp; English.

CC The invention relates to an antisense compound (I) 8-30 nucleobases in
 CC length targeted to a nucleic acid molecule encoding lysophospholipase I
 CC (II), where (I) specifically hybridises with and inhibits the expression
 CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
 CC and cardiovascular disorders such as atherosclerosis and myocardial
 CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway. (I) is useful in antisense gene therapy. AAU85132-AAU85136
 CC represent lysophospholipase I amino acid sequences of the invention.

XX Sequence 230 AA:

Query Match 88.5%; Score 947; DB 23; Length 230;

Best Local Similarity 80.4%; Pred. No. 2e-100;

Matches 185; Conservative 8; Mismatches 15; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTG-----PVRP 38
 DB 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTGHWAEAFAGIKSPHIKYPHAPVP 60
 QY 39 VTLNMMNVPMSWDITGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 DB 61 VTLNMMNVPMSWDITGLSPDSQEDSGIKQAETVYKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGALSTLTALTTOOKLAGVATLSFLPLRXSPQGPFGANRDISILQCHGCDPLVPLM 158
 DB 121 GGALSTLTALTTOOKLAGVATLSFLPLRXSPQGPFGANRDISILQCHGCDPLVPLM 180
 QY 159 FGSILTVEKLTIVNPAVNTFKTYEGMMHSSCOQEMMDVKQFTDKLLPID 208
 DB 181 FGSILTVEKLTIVNPAVNTFKTYEGMMHSSCOQEMMDVKQFTDKLLPID 230

RESULT 12

AAU828796
 ID AAB28796 standard; Protein; 231 AA.

XX AC AAB28796;

DT 13-FEB-2001 (first entry)

DE Human hydrolase-like molecule 7 protein.

XX Hydrolase-like molecule; human; cell proliferation disorder;
 KW autoimmune; cancer; AIDS; acquired immune deficiency syndrome.

XX Homo sapiens.

XX US6132964-A.

XX 17-OCT-2000.

XX 06-FEB-1998; 98US-0013881.

XX 06-FEB-1998; 98US-0013881.

XX (INCY-) INCYTE PHARM INC.

XX Bandman O, Hillman JL, Guegler KJ, Shah P, Lal P, Corley NC;

XX WPI; 2001-006133/01.

DR N-PSDB; AAC60229.

PT New human hydrolase-like molecules (HILMs) and polynucleotides encoding
 PT the HILMs, useful for diagnosing, treating or preventing cell
 PT proliferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or
 PT asthma)

XX Claim 1; Column 53-54; 38pp; English.
 PS The present invention relates to isolated and purified cDNA encoding a
 CC human hydrolase-like molecule (HLM), designated HLM-1 to HLM-8. The
 CC HLM DNAs and polypeptides are useful for diagnosing, treating or
 CC preventing cell proliferation disorders and autoimmune disorders. Cell
 CC proliferation disorders include cancers, autoimmune disorders include
 CC AIDS (acquired immune deficiency syndrome). The present sequence
 CC is a HLM protein of the invention.
 XX
 XX Sequence 231 AA;
 SQ
 Query Match 66.6%; Score 713; DB 22; Length 231;
 Best Local Similarity 60.8%; Pred. No. 1.8e-73;
 Matches 141; Conservative 28; Mismatches 37; Indels 26; Gaps 3;
 OY 1 MCGNNSTPL--PAIVPAARKATAAVIFLHGLDGTG-----P 35
 DB 1 MCGNTSVPLLTDAATVSGAERETAIVFLHGLDGTGSMADALSTRLPVHKYICPNAP 60
 OY 36 VRVVTNNMVAWMSWEDDIIIGLSPDSQDESGIKQAENIKALIDQVKNIGPSNRITLGG 95
 DB 61 RIVPTLNMKVMPSWFDLMLGSLPDAPEDEAGIKKAENIKALIEHMKNGITANRIVLGG 120
 OY 96 FSGGALSTYTLATTOOKLAGVTALSFLLPLRXSPQGPFGANRDISILQCHGDCDPLV 155
 DB 121 FSGGALSTYTLATTCCHPLAGIALSCWLPRLHRAFPQANGSA-KDLATLQCHGELDPV 179
 OY 156 PLMGSLTVEKLTLPANAVTEFKYEGMMHSSCOQEMDVKOFIDKLLPI 207
 DB 180 PVRFGLTAETKLRVTPAVCPKFTYRGVHSSCPQEMAIVKFELEKLLPV 231

RESULT 13
 ABB67341
 ID ABB67341 standard; Protein; 216 AA.
 XX
 AC ABB67341;
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 28815.
 XX
 KW Drosophila: developmental biology; cell signalling; insecticide;
 XX pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR
 DR N-PSDB; ABL11444.
 PT
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 28815; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72027).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 XX Sequence 216 AA;
 SQ
 Query Match 45.8%; Score 490; DB 22; Length 216;
 Best Local Similarity 48.1%; Pred. No. 7.9e-48;
 Matches 103; Conservative 24; Mismatches 61; Indels 26; Gaps 3;
 OY 11 PAIVPAARKATAAVIFLHGLDGTG-----PVRVTLNMVAWMP 48
 DB 4 PVIYDAIVKQRTILFMHGLDGTGHSMSALAIRPFPMKYICPTAPTOPVSLNAGFRMP 63
 OY 49 SWFDIIGLSPDSQDESGIKQAENIKALIDQVKNIGPSNRITLGGFSGGALSTYTL 108
 DB 64 SWFDLKTLDIGGPEDEPGIQAARDVHGMIOKEISAGIPANRIVLGGFSGGALATYSAL 123
 OY 109 TTOOKLAGVTALSFLLPLRXSPQGPFGANRDISILQCHGDCDPLVPLMGSLTVEK 168
 DB 124 TYDQPLAGVVALSCWLPKHQKPGAKVN--SDVPIFQAHDGYDPVPYKFGQLSASL 181
 OY 169 TLVNPAVTEFKYEGMMHSSCOQEMDVKOFIDK 202
 DB 182 SFMK--NTYFKTYSGLSHSSSDDEMDVDKDIISK 213

RESULT 14
 AAY48392
 ID AAY48392 standard; Protein; 119 AA.
 XX
 AC AAY48392;
 DT 08-DEC-1999 (first entry)
 XX
 DE Human prostate cancer-associated protein 89.
 XX
 KW Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;
 KW cancer; tissue specificity; human.
 XX
 OS Homo sapiens.
 XX
 PN DE19811194-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 10-MAR-1998; 98DE-1011194.
 XX
 PR 10-MAR-1998; 98DE-1011194.
 XX
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
 XX
 DR WPI: 1999-519629/44.
 DR
 DR N-PSDB; AA23516.
 PT
 PT New nucleic acid expressed at high level in normal prostatic tissue and
 PT encoded polypeptides, used to treat cancer and screen for therapeutic
 PT agents -
 XX
 PS Claim 22; 158; 194pp; German.
 XX
 CC This invention describes novel nucleic acid sequences (A) that are
 CC expressed at high level in normal prostatic tissue. Polypeptides (I)
 CC encoded by (A) are used: (a) for identifying agents for treatment of
 CC prostatic cancer and (b) for therapy of prostate cancer, optionally

CC where expressed by gene therapy methods. (A) is also used to isolate
 CC full-length genes (for gene therapy) and for recombinant production of
 CC (I), which can be used to raise specific antibodies. (A) are identified
 CC by assembly of ESTs (expressed sequence tags) before these are analyzed
 CC for expression pattern (tissue specificity). This approach eliminates
 CC many of the false results, as regards tissue specificity, associated
 CC with known methods that use single (usually short) ESTs. AA48304-Y48456
 CC represent peptides encoded by the expressed sequence tags described in
 CC the method of the invention.

XX Sequence 119 AA;

Query Match 38.0%; Score 406.5; DB 20; Length 119;
 Best Local Similarity 64.2%; Pred. No. 1.3e-38;
 Matches 77; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

OY 88 SNRIILGFSOGGALSLYALTTOOKLAGVYALSLPLLRXSPFGPIGANDISILQC 147
 Db 1 ANRIYLGFSOGGALSLYALTTCPHLAGIYALSCWLP LHRAPFOANGSA-KDLAILQC 59
 OY 148 HGDCDPLVPLMEGSLVEKTKTIYVNAVPEKTEGMMHSSCOEEMDVQOFIDKLPI 207
 Db 60 HGEIDPMVPVRFGALTAEKLSVTPARVOPKTPGVHSHSCPEMAVAEPELEKLLPV 119

RESULT 15

ABG07276
 ID ABG07276 standard; Protein: 89 AA.

XX AC ABG07276;

DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #7267.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS71463.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

XX PS Claim 20; SEQ ID NO 37635; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical

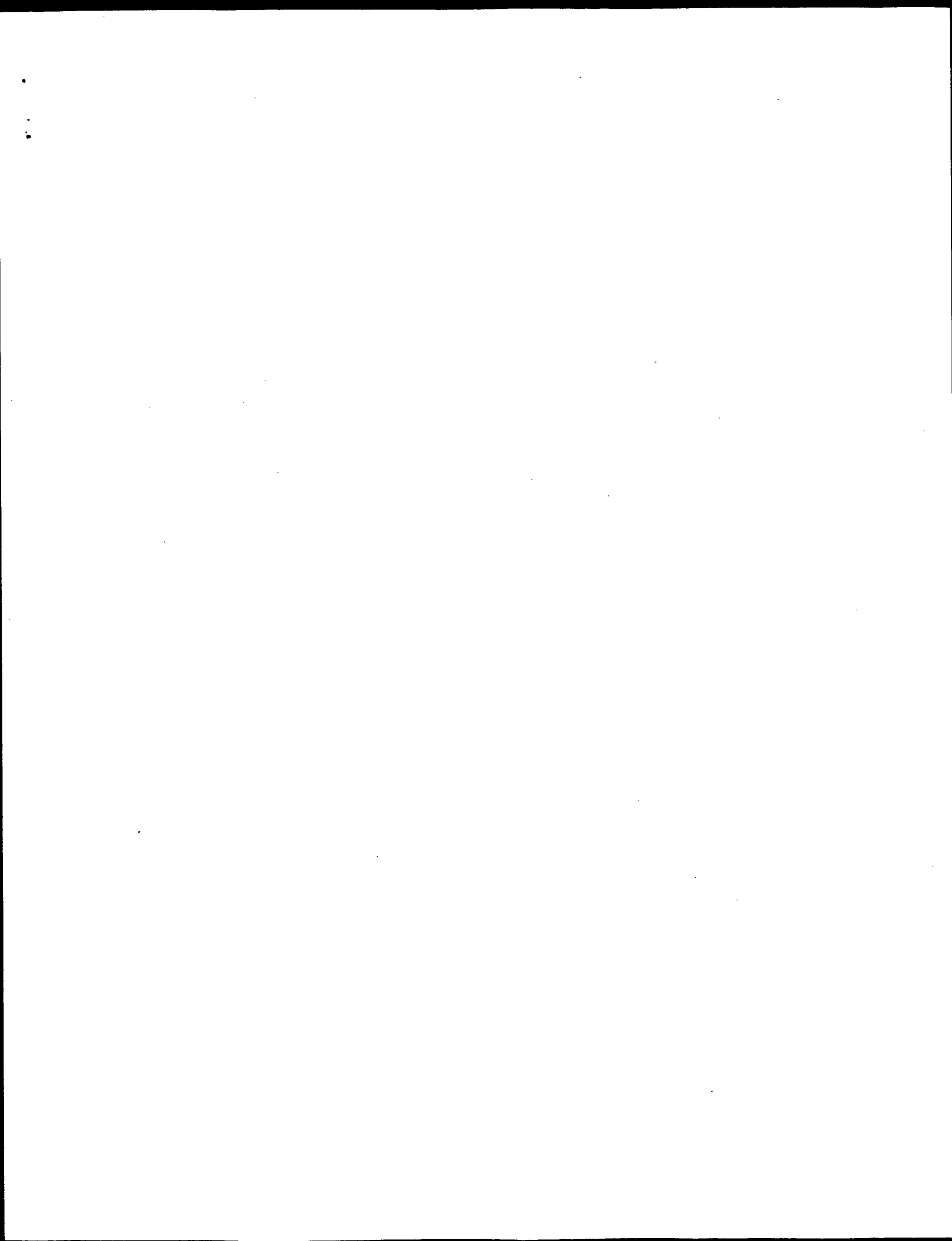
CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pot_sequences.

XX Sequence 89 AA;

Query Match 33.3%; Score 356; DB 22; Length 89;
 Best Local Similarity 73.3%; Pred. No. 5.7e-33;
 Matches 77; Conservative 2; Mismatches 10; Indels 16; Gaps 2;

OY 6 MSTPLPAIVPARKKATAAVIFLHGLDGTGPVPRVTLNMNVAMPSPFDIIGLSPSOEDS 65
 Db 1 MSAPLPAIVPATKATPAVIFLHGLDGTG-----HRWLEAFA--DSQEDP 44
 OY 66 GIKQAAMNIKALIDQEVKNGIPSNRIILGFSOGGALSLYALT 110
 Db 45 GIKQAAMNIKALIDQEVKNGIPSNRIILGFSOGGALSLYALT 89

Search completed: January 19, 2003, 03:19:39
 Job time : 142 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2003, 03:17:20 ; Search time 37 Seconds
(Without alignments)
165.405 Million cell updates/sec

Title: US-09-988-982-1

Perfect score: 1070

Sequence: 1 MCGNNMSTPLPAIVPARKA.....COEEMDVKQFIDKLEPID 208

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	1068	99.8	208	2	US-08-844-120-1	Sequence 1, Appl	
	2	1068	99.8	208	4	US-09-213-394-1	Sequence 1, Appl	
	3	1055	98.6	207	2	US-09-022-940-1	Sequence 1, Appl	
	4	1055	98.6	207	3	US-09-216-386-1	Sequence 1, Appl	
	5	1034	96.6	230	2	US-09-022-940-3	Sequence 3, Appl	
	6	1034	96.6	230	3	US-09-216-386-3	Sequence 3, Appl	
	7	958	89.5	230	2	US-08-844-120-3	Sequence 3, Appl	
	8	958	89.5	230	2	US-09-022-940-5	Sequence 5, Appl	
	9	958	89.5	230	3	US-09-216-001-3	Sequence 3, Appl	
	10	958	89.5	230	3	US-09-216-386-5	Sequence 5, Appl	
	11	958	89.5	230	4	US-08-878-862-3	Sequence 3, Appl	
	12	958	89.5	230	4	US-09-213-394-3	Sequence 3, Appl	
	13	713	66.6	231	4	US-09-013-881-7	Sequence 7, Appl	
	14	245	22.9	218	3	US-09-216-001-4	Sequence 4, Appl	
	15	245	22.9	218	4	US-08-878-862-4	Sequence 4, Appl	
	16	227.5	21.3	237	3	US-09-216-001-1	Sequence 1, Appl	
	17	227.5	21.3	237	4	US-08-878-862-1	Sequence 1, Appl	
	18	81.5	7.6	358	1	US-08-034-650-10	Sequence 10, Appl	
	19	81.5	7.6	358	1	US-08-449-015-10	Sequence 10, Appl	
	20	81.5	7.6	1005	4	US-09-770-170-4	Sequence 4, Appl	
	21	79	7.4	400	4	US-09-390-234-19	Sequence 19, Appl	
	22	79	7.4	400	4	US-09-390-234-22	Sequence 22, Appl	
	23	79	7.4	560	2	US-08-756-317-8	Sequence 8, Appl	
	24	78	7.3	267	3	US-08-935-263-10	Sequence 10, Appl	
	25	78	7.3	267	4	US-09-594-185-10	Sequence 10, Appl	
	26	77.5	7.2	252	4	US-09-134-001C-5644	Sequence 5644, Appl	
	27	77	7.2	1719	2	US-08-459-568-4	Sequence 4, Appl	

28	77	7.2	1719	2	US-08-399-411-4	Sequence 4, Appl
29	77	7.2	1719	3	US-08-516-859A-4	Sequence 4, Appl
30	77	7.2	1719	4	US-09-586-472-4	Sequence 4, Appl
31	77	7.2	1719	4	US-09-528-706-4	Sequence 4, Appl
32	76.5	7.1	256	4	US-09-355-166-2	Sequence 2, Appl
33	76	7.1	353	3	US-08-978-589A-2	Sequence 2, Appl
34	76	7.1	895	4	US-08-827-962-19	Sequence 19, Appl
35	76	7.1	895	4	US-08-827-962-21	Sequence 21, Appl
36	76	7.1	1162	4	US-08-827-962-15	Sequence 15, Appl
37	76	7.1	1162	4	US-08-827-962-20	Sequence 20, Appl
38	76	7.1	1162	4	US-08-803-346-1	Sequence 1, Appl
39	75.5	7.1	346	2	US-08-602-359A-34	Sequence 34, Appl
40	75.5	7.1	363	4	US-09-336-601-1	Sequence 1, Appl
41	75.5	7.1	373	4	US-09-039-198A-14	Sequence 14, Appl
42	75.5	7.1	373	4	US-09-039-198A-15	Sequence 15, Appl
43	75.5	7.1	373	4	US-08-877-599-14	Sequence 14, Appl
44	75.5	7.1	373	4	US-08-877-599-15	Sequence 15, Appl
45	75.5	7.1	373	4	US-09-267-574-14	Sequence 14, Appl

ALIGNMENTS

```
RESULT 1
US-08-844-120-1
; Sequence 1, Application US/08844120
; Patent No. 5858756
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Puri
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,120
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT19
; CLONE: 267650
; US-08-844-120-1

Query Match 99.8%; Score 1068; DB 2; Length 208;
Best local Similarity 100.0%; Pred. No. 6.8e-118;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCGNNMSTPLPAIVPARKATAVIFLHGIIGDTPVRYPTLNNNVAMPSPFIDIGLSPDS 60
Db 1 MCGNNMSTPLPAIVPARKATAVIFLHGIIGDTPVRYPTLNNNVAMPSPFIDIGLSPDS 60
```

121 SPLEENKASERFÜR 100MMK101EUCNOD
QY

RESULT 4

RESULT 4

```

US-09-216-386-1
; Sequence 1, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-216-386-1
Query Match          98.6%; Score 1055; DB 3; Length 207;
Best Local Similarity 99.5%; Pred. No. 2.3e-116;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCGNNMSTPLPAIPAAKATAAIVFLHGLDGTGVRPVTLMNMYAMPSPWDIIGLSPDS 60
DB 1 MCGNNMSTPLPAIPAAKATAAIVFLHGLDGTGVRPVTLMNMYAMPSPWDIIGLSPDS 60
QY 61 QDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGGALSYTALTTOOKLAGVTAL 120
DB 61 QDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGGALSYTALTTOOKLAGVTAL 120
QY 121 SFLLPLRXSFPGPIGKANRDISILOCHGDCDPLVPLMFGSLTYEKLTLVNPANVTPEKT 180
DB 121 SFLLPLRXSFPGPIGKANRDISILOCHGDCDPLVPLMFGSLTYEKLTLVNPANVTPEKT 180
QY 181 YEGMHSSCOQEMDMVKOFIDKLPPID 207
DB 181 YEGMHSSCOQEMDMVKOFIDKLPPID 207

RESULT 5
US-09-022-940-3
; Sequence 3, Application US/09022940
; Patent No. 5965423
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,940
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-022-940-3
Query Match          96.6%; Score 1034; DB 2; Length 230;
Best Local Similarity 89.1%; Pred. No. 8.2e-114;
Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIPAAKATAAIVFLHGLDGTG-----PVPR 38
DB 1 MCGNNMSTPLPAIPAAKATAAIVFLHGLDGTG-----PVPR 38
QY 39 VTLNMYAMPSPWDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 98
DB 61 VTLNMYAMPSPWDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 120
QY 99 GALSILYALTTOOKLAGVTALSFLLPLRXSFPGPIGKANRDISILOCHGDCDPLVPLM 158
DB 121 GALSILYALTTOOKLAGVTALSCWPLPLRASFPQPIGKANRDISILOCHGDCDPLVPLM 180
QY 159 FGSILTYEKLTLVNPANVTPEKT YEGMHSSCOQEMDMVKOFIDKLPPID 208
DB 181 FGSILTYEKLTLVNPANVTPEKT YEGMHSSCOQEMDMVKOFIDKLPPID 230

RESULT 6
US-09-216-386-3
; Sequence 3, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,386
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-216-386-3

Query Match 96.6%; Score 1034; DB 3; Length 230;
Best Local Similarity 89.1%; Pred. No. 8.2e-114;
Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIYPARKATAVIFLHGLDPTG-----PVRP 38
DB 1 MCGNNMSTPLPAIYPARKATAVIFLHGLDPTGHNAAEAFAGIRSHIKYICPHAPVRP 60
QY 39 VTLNMMNVAMPSPWFIDIIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 98
DB 61 VTLNMMNVAMPSPWFIDIIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 120
QY 99 GGALSLYTLTLOOKLAGVTALSFLLPLRXSPQGPIGGANDISILQCHGDCDPLVPLM 158
DB 121 GGALSLYTLTLOOKLAGVTALSCWPLRLASFPQGPIGGANDISILQCHGDCDPLVPLM 180
QY 159 FGSILTVKRLTLVNPANVTFTKYEEMHSSCOQEMMDVKQFIDKLLPPID 208
DB 181 FGSILTVKRLTLVNPANVTFTKYEEMHSSCOQEMMDVKQFIDKLLPPID 230

RESULT 7
US-08-844-120-3
Sequence 3, Application US/08844120
Patent No. 5858756
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 552244
US-08-844-120-3

Query Match 89.5%; Score 958; DB 2; Length 230;
Best Local Similarity 81.7%; Pred. No. 7.5e-105;
Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIYPARKATAVIFLHGLDPTG-----PVRP 38
DB 1 MCGNNMSTPLPAIYPARKATAVIFLHGLDPTGHNAAEAFAGIRSHIKYICPHAPVRP 60
QY 39 VTLNMMNVAMPSPWFIDIIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 98
DB 61 VTLNMMNVAMPSPWFIDIIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSQ 120
QY 99 GGALSLYTLTLOOKLAGVTALSFLLPLRXSPQGPIGGANDISILQCHGDCDPLVPLM 158
DB 121 GGALSLYTLTLOOKLAGVTALSCWPLRLASFPQGPIGGANDISILQCHGDCDPLVPLM 180
QY 159 FGSILTVKRLTLVNPANVTFTKYEEMHSSCOQEMMDVKQFIDKLLPPID 208
DB 181 FGSILTVKRLTLVNPANVTFTKYEEMHSSCOQEMMDVKQFIDKLLPPID 230

RESULT 8
US-09-022-940-5
Sequence 5, Application US/09022940
Patent No. 5965423
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,940
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 230 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-022-940-5

Query Match 89.5%; Score 958; DB 2; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.5e-105;
 Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;

QY 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTG-----PVPR 38
 DB 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTGHEAFAGIKSHIKYICPHAPVMP 60
 QY 39 VTLNNVAMPSPWFIDIGLSPDSQEDSGIKQAENIKALIDQEVKNKNGIPSNRIILGGFSQ 98
 DB 61 VTLNNVAMPSPWFIDIGLSPDSQEDSGIKQAETVAKALIDQEVKNKNGIPSNRIILGGFSQ 120
 QY 99 GGALSLYTALTTOOKLAGVTALSFLLPLRXSPQGPIGGANDRISILQCHGDCDPLVPLM 158
 DB 121 GGALSLYTALTTOOKLAGVTALSCWPLRASFSGPINSANRDISVLQCHGDCDPLVPLM 180
 QY 159 FGSLLVEKLTIVPANVTFTYEGMMHSSCOQEMMDVKYFIDKLLPPID 208
 DB 181 FGSLLVEKLTIVPANVTFTYEGMMHSSCOQEMMDVKYFIDKLLPPID 230

RESULT 9

Sequence 3, Application US/09216001
 Patent No. 6004792

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
 APPLICANT: Shah, Purvi
 APPLICANT: Corley, Neil C.
 APPLICANT: Murry, Lynn E.
 TITLE OF INVENTION: NEW HUMAN LYOPHOSPHOLIPASE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESS: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/216.001
 FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/878,862
 FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0329 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 230 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank

CLONE: 1552244
 US-09-216-001-3

Query Match 89.5%; Score 958; DB 3; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.5e-105;
 Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;

QY 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTG-----PVPR 38
 DB 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTGHEAFAGIKSHIKYICPHAPVMP 60
 QY 39 VTLNNVAMPSPWFIDIGLSPDSQEDSGIKQAENIKALIDQEVKNKNGIPSNRIILGGFSQ 98
 DB 61 VTLNNVAMPSPWFIDIGLSPDSQEDSGIKQAETVAKALIDQEVKNKNGIPSNRIILGGFSQ 120
 QY 99 GGALSLYTALTTOOKLAGVTALSFLLPLRXSPQGPIGGANDRISILQCHGDCDPLVPLM 158
 DB 121 GGALSLYTALTTOOKLAGVTALSCWPLRASFSGPINSANRDISVLQCHGDCDPLVPLM 180
 QY 159 FGSLLVEKLTIVPANVTFTYEGMMHSSCOQEMMDVKYFIDKLLPPID 208
 DB 181 FGSLLVEKLTIVPANVTFTYEGMMHSSCOQEMMDVKYFIDKLLPPID 230

RESULT 10

Sequence 5, Application US/09216386
 Patent No. 603561

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
 APPLICANT: Shah, Purvi
 APPLICANT: Murry, Lynn E.
 TITLE OF INVENTION: HUMAN LYOPHOSPHOLIPASE
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESS: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/216.386
 FILING DATE:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/022,940
 FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 230 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-216-386-5

Query Match 89.5%; Score 958; DB 3; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.5e-105;
 Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;
 QY 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTG-----PVPR 38
 DB 1 MCGNNSTPLPAIVPAARKATAVIFLHGLGDTG-----PVPR 38

Db 1 MCGNNNSAPMPAVPAARKATAVIFLHGLDPTGHWAEAFAGIKSSHIKICPHAPVMP 60
 QY 39 VTLNMMVAMPWFDDIIGLSPDSEDSEGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 Db 61 VTLNMMVAMPWFDDIIGLSPDSEDSEGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGLSLYLTALTTOOKLAGVTALSFLLPLRXSFPQGPFGIGANDRISILQCHGDCDPLVPLM 158
 Db 121 GGLSLYLTALTTOOKLAGVTALSCWPLRXASFSGPINSANRDISVLQCHGDCDPLVPLM 180
 QY 159 FGSILVEKLKTLVNPANVTFFKTYEGMMHSSCOQEMMDVKQFIDKLPLPID 208
 Db 181 FGSILVEKLKTLVNPANVTFFKTYEGMMHSSCOQEMMDVKQFIDKLPLPID 230

RESULT 11

US-08-878-862-3
 ; Sequence 3, Application US/08878862
 ; Patent No. 6143544
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/878,862
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0329 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 230 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1552244
 ; US-08-878-862-3
 Query Match 89.5%; Score 958; DB 4; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.5e-105;
 Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;
 QY 1 MCGNNNSAPMPAVPAARKATAVIFLHGLDPTGHWAEAFAGIKSSHIKICPHAPVMP 38
 Db 1 MCGNNNSAPMPAVPAARKATAVIFLHGLDPTGHWAEAFAGIKSSHIKICPHAPVMP 60
 QY 39 VTLNMMVAMPWFDDIIGLSPDSEDSEGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 98

Db 61 VTLNMMVAMPWFDDIIGLSPDSEDSEGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGLSLYLTALTTOOKLAGVTALSFLLPLRXSFPQGPFGIGANDRISILQCHGDCDPLVPLM 158
 Db 121 GGLSLYLTALTTOOKLAGVTALSCWPLRXASFSGPINSANRDISVLQCHGDCDPLVPLM 180
 QY 159 FGSILVEKLKTLVNPANVTFFKTYEGMMHSSCOQEMMDVKQFIDKLPLPID 208
 Db 181 FGSILVEKLKTLVNPANVTFFKTYEGMMHSSCOQEMMDVKQFIDKLPLPID 230

RESULT 12

US-09-213-394-3
 ; Sequence 3, Application US/09213394
 ; Patent No. 6319701
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Murry, Lynn E.
 ; TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/213,394
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/844,120
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0269 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 230 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 552244
 ; US-09-213-394-3
 Query Match 89.5%; Score 958; DB 4; Length 230;
 Best Local Similarity 81.7%; Pred. No. 7.5e-105;
 Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;
 QY 1 MCGNNNSAPMPAVPAARKATAVIFLHGLDPTGHWAEAFAGIKSSHIKICPHAPVMP 38
 Db 1 MCGNNNSAPMPAVPAARKATAVIFLHGLDPTGHWAEAFAGIKSSHIKICPHAPVMP 60
 QY 39 VTLNMMVAMPWFDDIIGLSPDSEDSEGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 Db 61 VTLNMMVAMPWFDDIIGLSPDSEDSEGIKQAAETVKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGLSLYLTALTTOOKLAGVTALSFLLPLRXSFPQGPFGIGANDRISILQCHGDCDPLVPLM 158
 Db 121 GGLSLYLTALTTOOKLAGVTALSCWPLRXASFSGPINSANRDISVLQCHGDCDPLVPLM 180

OY 159 FGSITVEKLTLYNPANVTFTYEGMHSSCOQEMMDVKOFIDKLLPPI 208
 DB 181 FGSITVEKLTLYNPANVTFTYEGMHSSCOQEMMDVKOFIDKLLPPI 230

RESULT 13

US-09-013-881-7
 ; Sequence 7, Application US/09013881
 ; Patent No. 6132964
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/013,881
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BILLINGS, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0470 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 231 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: COLANOT02
 ; CLONE: 2768301
 ; US-09-013-881-7

Query Match 66.6%; Score 713; DB 4; Length 231;
 Best Local Similarity 60.8%; Pred. No. 6e-76;
 Matches 141; Conservative 28; Mismatches 37; Indels 26; Gaps 3;

OY 1 MCGNMSTPL---PAIYPAARKATAAIVFLHGLDGTG-----P 35
 DB 1 MCGNMSTPLLTDAATVSGAERETAAVFLHGLDGTGSHWADALSTRPLPHVKYICPHAP 60
 OY 36 VRPVTLLNNVAMPWFIDIGLSPDOEDSGIKOAENIKALIDOEYKNGIPSRNIIIG 95
 DB 61 RIVPTLNNKVMWPFIDMGISPDAPDEAGIKKAENIKALIHHEKNGIPARIVIG 120
 OY 96 FSGGALSILYALITQKLAGVTLSTLLPLRXSFPQGPFGGANDISITLQCHGDCDPLV 155
 DB 121 FSGGALSILYALITQKLAGVTLSTLLPLRXSFPQGPFGGANDISITLQCHGDCDPLV 179

OY 156 PLMFSLTVEKLTLYNPANVTFTYEGMHSSCOQEMMDVKOFIDKLLPPI 207
 DB 180 PVRFGLTAEKLSVYTPARVQFRTYPGVHSSCPQEMAIVAEFLKLLPVP 231

RESULT 14

US-09-216-001-4
 ; Sequence 4, Application US/09216001
 ; Patent No. 6004792
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Murty, Lynn E.
 ; TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/216,001
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/878,862
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BILLINGS, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0329 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 218 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 244501
 ; US-09-216-001-4

Query Match 22.9%; Score 245; DB 3; Length 218;
 Best Local Similarity 33.0%; Pred. No. 8.8e-21;
 Matches 70; Conservative 30; Mismatches 80; Indels 37; Gaps 6;

OY 11 PAIYPAARKATAAIVFLHGLG-----DTGVPVPTLLNNVNA 46
 DB 4 PLIIQPAKPADACVIMHGLGADRYDFMVAEALQESLITTRFVLPOAPRPVYINGVE 63
 OY 47 MPWFIDIGLSPDOEDSGIKOAENIKALIDOEYKNGIPSRNIIIGFSGGALSITV 106
 DB 64 MPWFIDIGLSPDOEDSGIKOAENIKALIDOEYKNGIPSRNIIIGFSGGALSITV 123
 OY 107 A-LTTOOKLAGVTLSTLLPLRXSF--PQGPFGGANDISITLQCHGDCDPLVPMFSLTV 164
 DB 124 AFTNMGPLGGLVTLSTYAP---TFGDELELSAQQRIPALCHGQYDDVYVQNAKRSAP 180
 OY 165 EKLKTLVNPANVTFTYEGMHSSCOQEMMDV 196
 DB 181 EHLKS--RGVTVTWQEYR--MGHEVLPQEIHDI 209

Job time : 58 secs

RESULT 15

US-08-878-862-4

; Sequence 4, Application US/08878862
; Patent No. 6143544

GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Shah, Purvi

; APPLICANT: Corley, Neil C.

; TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/878,862

; FILING DATE: Herewith

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0329 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 244501

; US-08-878-862-4

Query Match 22.9%; Score 245; DB 4; Length 218;

Best Local Similarity 33.0%; Pred. No. 8.8e-21; Matches 70; Conservative 30; Mismatches 80; Indels 32; Gaps 6;

QY 11 PAIVPAARKATAAVIFHIGL-----DTGPVRYPTLNMNVA 46

Db 4 PLIIQPAKRPADACYIWHGICADRYDEMVAEALQESLITTRVLPQAPTRPTINGYE 63

QY 47 MPWFIDILSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGALSLYT 106

Db 64 MPWYDIDIKAMSPARSISLELEYSAAKVVTDLEAKRTGIDASRIFLAGSGGAVVFHT 123

QY 107 A-LTQOKLAGVTALSLFLPLKRSF-PQGPFGANRDISILQCHGCDPLVPLMFSGLTY 164

Db 124 AFINMOGLGVIATLSTYAP--TFGDELELSASQCRIPALCLHGQYDDVYQANMGRSAF 180

QY 165 EKLTILVNPANTVEKTEGMMHSSCOQEMMDV 196

Db 181 EHLKS--RGVTVTWQETP-MGHEVLPQELHDI 209

Search completed: January 19, 2003, 03:25:56

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2003, 03:20:15 : Search time 75 Seconds
(without alignments)
55.130 Million cell updates/sec

Title: US-09-988-982-1
Perfect score: 1070
Sequence: 1 MCGNNMSTPLPAIVPARKA.....COQEMMDVKQIDKLPIID 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications-AA:*
1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1068	99.8	208	10	US-09-988-982-1
2	1034	96.6	263	10	US-09-925-299-991
3	958	89.5	230	10	US-09-988-982-3
4	521.5	48.7	236	9	US-09-934-392-4
5	89.5	8.4	219	9	US-09-791-171-14
6	86	8.0	197	10	US-09-815-242-5457
7	86	8.0	198	10	US-09-815-242-1680
8	81	7.6	226	10	US-09-791-171-52
9	81	7.6	322	10	US-09-815-242-11790
10	79.5	7.4	308	9	US-09-738-626-3637
11	79	7.4	217	10	US-09-791-171-10
12	79	7.4	262	10	US-09-791-171-56
13	78	7.3	267	12	US-10-033-078-10
14	77	7.2	310	9	US-09-934-392-2
15	76.5	7.1	256	10	US-09-950-368-2
16	75.5	7.1	346	9	US-10-027-805-34
17	75	7.0	891	9	US-09-976-059-18
18	74.5	7.0	285	9	US-10-051-643-197
19	74.5	7.0	308	10	US-09-999-162-2

20	74.5	7.0	346	10	US-09-903-410-34	Sequence 34, Appl
21	74	6.9	700	10	US-09-840-707A-9	Sequence 9, Appl
22	74	6.9	700	10	US-09-768-877-23	Sequence 23, Appl
23	73.5	6.9	297	9	US-10-027-805-37	Sequence 37, Appl
24	73.5	6.9	297	10	US-09-903-410-37	Sequence 37, Appl
25	73.5	6.9	354	10	US-09-999-162-14	Sequence 14, Appl
26	73	6.8	601	10	US-09-815-242-5070	Sequence 5070, Ap
27	72.5	6.8	271	9	US-09-738-626-6380	Sequence 6380, Ap
28	72.5	6.8	331	9	US-09-738-626-3832	Sequence 3832, Ap
29	72	6.7	200	10	US-09-815-242-10705	Sequence 10705, A
30	72	6.7	1053	10	US-09-815-242-5136	Sequence 5136, Ap
31	69.5	6.5	262	9	US-10-027-805-38	Sequence 38, Appl
32	69.5	6.5	262	10	US-09-903-410-38	Sequence 38, Appl
33	69.5	6.5	416	10	US-09-805-848A-2	Sequence 2, Appl
34	69.5	6.5	416	10	US-09-805-848A-4	Sequence 4, Appl
35	69.5	6.5	655	9	US-10-117-641-36	Sequence 36, Appl
36	69.5	6.5	1062	10	US-09-815-242-5111	Sequence 5111, Ap
37	69	6.4	300	10	US-09-794-960-5	Sequence 5, Appl
38	68.5	6.4	167	9	US-10-051-643-112	Sequence 112, App
39	68.5	6.4	167	9	US-09-880-505-112	Sequence 112, App
40	68.5	6.4	232	10	US-09-896-578-4	Sequence 4, Appl
41	68.5	6.4	247	9	US-09-738-626-6438	Sequence 6438, Ap
42	68.5	6.4	271	9	US-09-976-059-10	Sequence 10, Appl
43	68.5	6.4	748	9	US-10-051-643-154	Sequence 154, App
44	68.5	6.4	748	9	US-09-880-505-154	Sequence 154, App
45	68	6.4	229	10	US-09-879-957-221	Sequence 221, App

ALIGNMENTS

RESULT 1
US-09-988-982-1
Sequence 1, Application US/09988982
Patent No. US20020081699A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Murry, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,982
FILING DATE: 19-NO. US20020081699A1-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/213,394
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

LIBRARY: KIDNOT19
CLONE: 2676650
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-988-982-1

Query Match 99.8%; Score 1068; DB 10; Length 208;
Best Local Similarity 100.0%; Pred. No. 1,7e-108;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGNNSTPLPAIVPAARAKATAVIFLHGLGDTGPRPTLVNMANVAMPSPEDIIIGLSPDS 60
DB 1 MCGNNSTPLPAIVPAARAKATAVIFLHGLGDTGPRPTLVNMANVAMPSPEDIIIGLSPDS 60
QY 61 QEDDSGIKQAEENIKALIDQEVKNGIPSNRIILGFSOGGALSITYALTTOOKLAGVTAL 120
DB 61 QEDDSGIKQAEENIKALIDQEVKNGIPSNRIILGFSOGGALSITYALTTOOKLAGVTAL 120
QY 121 SFLLPLRXSFPOGPIGANDISIILOCHGDCDPLVPLMGSLTVEKTLVNPANVTFT 180
DB 121 SFLLPLRXSFPOGPIGANDISIILOCHGDCDPLVPLMGSLTVEKTLVNPANVTFT 180
QY 181 YEGMHSSCOQEMMDVKOFIDKLLPPID 208
DB 181 YEGMHSSCOQEMMDVKOFIDKLLPPID 208

RESULT 2

US-09-925-299-991
Sequence 991, Application US/09925299
Patent No. US20020055627A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 991
LENGTH: 263
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-991

Query Match 96.6%; Score 1034; DB 10; Length 263;
Best Local Similarity 89.1%; Pred. No. 1.2e-104;
Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MCGNNSTPLPAIVPAARAKATAVIFLHGLGDTG-----PVRP 38
DB 34 MCGNNSTPLPAIVPAARAKATAVIFLHGLGDTGHWMAEAFAGIKSSHIIKICPHAVVP 93
QY 39 VTLNMANVAMPSPEDIIIGLSPDSQEDDSGIKQAEENIKALIDQEVKNGIPSNRIILGFSQ 98
DB 94 VTLNMANVAMPSPEDIIIGLSPDSQEDDSGIKQAEENIKALIDQEVKNGIPSNRIILGFSQ 153
QY 99 GGALSITYALTTOOKLAGVTALSFLLPLRXSFPOGPIGANDISIILOCHGDCDPLVPLM 158
DB 154 GGALSITYALTTOOKLAGVTALSCWLPRLASFPOGPIGANDISIILOCHGDCDPLVPLM 213
QY 159 FGSILTVEKTLVNPANVTFTYEGMHSSCOQEMMDVKOFIDKLLPPID 208
DB 214 FGSILTVEKTLVNPANVTFTYEGMHSSCOQEMMDVKOFIDKLLPPID 263

RESULT 3

US-09-988-982-3
Sequence 3, Application US/09988982
Patent No. US20020081699A1

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Murry, Lynn E.

TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,982
FILING DATE: 19-No. US20020081699A1-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/213,394

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 552244

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-988-982-3

Query Match 89.5%; Score 958; DB 10; Length 230;
Best Local Similarity 81.7%; Pred. No. 1.8e-96;
Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;

QY 1 MCGNNSTPLPAIVPAARAKATAVIFLHGLGDTG-----PVRP 38
DB 1 MCGNNMSPMPAVVPAARAKATAVIFLHGLGDTGHWMAEAFAGIKSSHIIKICPHAVVP 60
QY 39 VTLNMANVAMPSPEDIIIGLSPDSQEDDSGIKQAEENIKALIDQEVKNGIPSNRIILGFSQ 98
DB 61 VTLNMANVAMPSPEDIIIGLSPDSQEDDSGIKQAEATVATLIDQEVKNGIPSNRIILGFSQ 120
QY 99 GGALSITYALTTOOKLAGVTALSFLLPLRXSFPOGPIGANDISIILOCHGDCDPLVPLM 158
DB 121 GGALSITYALTTOOKLAGVTALSCWLPRLASFPOGPIGANDISIILOCHGDCDPLVPLM 180
QY 159 FGSILTVEKTLVNPANVTFTYEGMHSSCOQEMMDVKOFIDKLLPPID 208
DB 181 FGSILTVEKTLVNPANVTFTYEGMHSSCOQEMMDVKOFIDKLLPPID 230

RESULT 4

US-09-934-392-4
Sequence 4, Application US/09934392
Patent No. US20020155497A1

GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38618, A NOVEL HUMAN ALPHA/BETA
HYDROLASE FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-082001

```

: CURRENT APPLICATION NUMBER: US/09/934,392
: CURRENT FILING DATE: 2001-08-21
: PRIOR APPLICATION NUMBER: 60/226,737
: PRIOR FILING DATE: 2000-08-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 236
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Consensus sequence
US-09-934-392-4

```

```

Query Match          48.7%; Score 521.5; DB 9; Length 236;
Best Local Similarity 50.6%; Pred. No. 4.5e-49;
Matches 118; Conservative 17; Mismatches 59; Indels 39; Gaps 3;

```

```

QY 11 PAIVPAKATAAVIFLHGLDGTG-----PVRPTLMN 44
    ||| | | | | | | | | | | | | | | | | | | |
DB 4 PAIVPAKATAAVIFLHGLDGTGHWYGNAPAKTEALPNTKFIIPHAPEITVLNG 63
    ||| | | | | | | | | | | | | | | | | | | |
QY 45 VAPSWPILIGLSPDS-QEDSGIKQAENIKALIDQEVKNG-----IPSNRI 91
    ||| | | | | | | | | | | | | | | | | | | |
DB 64 RMPWAFDLEGISPEGLKDEAGIKNSAETIEELIDAEQKTKGKALEELILEIPSSRI 123
    ||| | | | | | | | | | | | | | | | | | | |
QY 92 ILGSGGALSLYATLTTQOKIAGVTALSFLLPLRXSPGCPICGANROISILQCHDC 151
    ||| | | | | | | | | | | | | | | | | | | |
DB 124 ILGSGGALSLYATLTPPLGILSLGALPLPKFPHPALAAVDPIILLIHGTE 183
    ||| | | | | | | | | | | | | | | | | | | |
QY 152 DPLVPLMGSLVLEKTLVNPANVTFTYEGMHSSCOQEMDVOKPFIKIL 204
    ||| | | | | | | | | | | | | | | | | | | |
DB 184 DPLVPLMGSLVLEKTLVNPANVTFTYEGMHSSCOQEMDVOKPFIKIL 236
    ||| | | | | | | | | | | | | | | | | | | |

```

```

RESULT 5
US-09-791-171-14
: Sequence 14, Application US/09791171
: Patent No. US20020094336A1
: GENERAL INFORMATION:
: APPLICANT: ANDERSEN, Peter
: APPLICANT: NIELSEN, Rikke
: APPLICANT: OETTINGER, Thomas
: APPLICANT: RASMUSSEN, Peter Birk
: APPLICANT: ROSENKRANDS, Ida
: APPLICANT: WEDDINGH, Karin
: APPLICANT: FLORIO, Walter
: TITLE OF INVENTION: NOCULEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
: FILE REFERENCE: 670001-2002.1
: CURRENT APPLICATION NUMBER: US/09/791,171
: CURRENT FILING DATE: 2001-02-20
: PRIOR APPLICATION NUMBER: 09/050,739
: PRIOR FILING DATE: 1998-03-30
: PRIOR APPLICATION NUMBER: 0376/97
: PRIOR FILING DATE: 1997-04-02
: PRIOR APPLICATION NUMBER: 1277/97
: PRIOR FILING DATE: 1997-11-10
: PRIOR APPLICATION NUMBER: 60/044,624
: PRIOR FILING DATE: 1997-04-18
: PRIOR APPLICATION NUMBER: 60/070,488
: PRIOR FILING DATE: 1998-01-05
: NUMBER OF SEQ ID NOS: 173
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 14
: LENGTH: 219
: TYPE: PRT
: ORGANISM: Mycobacterium tuberculosis
US-09-791-171-14

```

```

Query Match          8.4%; Score 89.5; DB 10; Length 219;
Best Local Similarity 28.3%; Pred. No. 0.033;
Matches 53; Conservative 21; Mismatches 60; Indels 53; Gaps 13;

```

```

QY 8 TPL--PAIVP-AARKATAA-----VIFLH-----GLDGTGPVRYVL-----NMNVAMPS 49
    ||| | | | | | | | | | | | | | | | | | | |
DB 15 TPLIVPAGYGAATAPATACPDAAEVYFARGRFEPPIGTYGNAFVSLRKYKKNVGYTA 74
    ||| | | | | | | | | | | | | | | | | | | |
QY 50 WFDIIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILGFSOGALS-LYAL 108
    ||| | | | | | | | | | | | | | | | | | | |
DB 75 ----VKYPADNO-----IDVGANDMSAHI-QSMANSCPNTRLVPGVSLGAATVDVLAV 124
    ||| | | | | | | | | | | | | | | | | | | |
QY 109 TTYQ-----QKLAGVIALSLFLPLRXSPGCPI-----GGANROISILQCHDC-- 150
    ||| | | | | | | | | | | | | | | | | | | |
DB 125 PLOMMGTTNPLPPGSDERHIAVALFG-----NSQWVGPITNSPAYNDRTIELCHGDDP 179
    ||| | | | | | | | | | | | | | | | | | | |
QY 151 -CDPLVP 156
    ||| | | | | | | | | | | | | | | | | | | |
DB 180 VCHPADP 186
    ||| | | | | | | | | | | | | | | | | | | |

```

```

RESULT 6
US-09-815-242-5457
: Sequence 5457, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Karl J.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 5457
: LENGTH: 197
: TYPE: PRT
: ORGANISM: Staphylococcus aureus
US-09-815-242-5457

```

```

Query Match          8.0%; Score 86; DB 10; Length 197;
Best Local Similarity 24.3%; Pred. No. 0.068;
Matches 41; Conservative 26; Mismatches 64; Indels 38; Gaps 7;

```

```

QY 24 VIFLHGL-GDTGPVRYV--TLNNNV-----AMPSWFDIIG-----LSPOS 60
    ||| | | | | | | | | | | | | | | | | | | |
DB 15 LILHGTGDEPDLPDLGALNENYHLLSIRGOVSENGMRRFKRLGSEGVYDEEDLAFRG 74
    ||| | | | | | | | | | | | | | | | | | | |
QY 61 QEDSGIKQAENIKALIDQEVKNGIPSNRIILGFSOGALSLYATLTTQOKIAGVTAL 120
    ||| | | | | | | | | | | | | | | | | | | |
DB 75 QELLTFIKAEAR-----YDFDIE-----KAVLYGFSNSGNSINAINMLSEAPFKKALLY 124
    ||| | | | | | | | | | | | | | | | | | | |
QY 121 SFLLPLRXSPGCPICGANROISILQCHDCDPLVPLMGFSLTVKTKT 169
    ||| | | | | | | | | | | | | | | | | | | |
DB 125 APYPIEVSTKN-----LSDVSVLLSMGKHDPYIPLAASEGVINLFTK 168
    ||| | | | | | | | | | | | | | | | | | | |

```

[illegible]

; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11790
; LENGTH: 322
; TYPE: PRF
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11790

Query Match 7.6%; Score 81; DB 10; Length 322;
Best Local Similarity 21.3%; Pred. No. 0.47; Indels 32; Gaps 7;

Matches 37; Conservative 33; Mismatches 72; Indels 32; Gaps 7;

QY 13 IYPAARKATAVFIHFG-AGDFGVPVPT-----LNNVAMPSPFDITIGLSPDSQ 61
DB 59 VPPGSEGAFLVYLHSGSGDQAMRISGIFDRLAAGEFLVAYPDGFE--GHNDCR 116
DB 62 E-----DESGIKOAEENIKALIDQEVKNGIPSRILIGFSOGALSLYTALT 110
DB 117 KASYSARLRDVEDVAFLRA--LVARLAQEYR--VDSQRYVAGYSGNGQAFRLAARA 171
QY 111 QOKLAGVTALSLFLPLRXSPGPIGANDRISILQCHDCDPLVPLMGSLTV 164
DB 172 PGLPAPAAIAVAASLPPTGTNDACRPV--BRPTAALLINSTRDPIINPYLGKVS 222

RESULT 10

US-09-738-626-3637
; Sequence 3637, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIRO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3637
; LENGTH: 308
; TYPE: PRF
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3637

Query Match 7.4%; Score 79.5; DB 9; Length 308;
Best Local Similarity 26.9%; Pred. No. 0.65;
Matches 29; Conservative 20; Mismatches 38; Indels 21; Gaps 4;

QY 24 VIFLHGLGDTGVPRVPTLMM-----NVAMPSPFDITIGLSPD-----SQDESGIKO 70
DB 74 LVYFHGGGSGC---TLNMDATVHSLVGLP-----ITLSVDYRLAPAFHPPAIDA 125
QY 71 AENIKALIDQEVKNGIPSRILIGFSOGALSLYTALTQOKLAGVT 118
DB 126 FAVVASVLVGGSLDSTRVALIGDSAGNIAVTAQDLRRRAVGST 173

RESULT 11

US-09-791-171-10
; Sequence 10, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WEIDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 10
; LENGTH: 217
; TYPE: PRF
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-10

Query Match 7.4%; Score 79; DB 10; Length 217;
Best Local Similarity 25.4%; Pred. No. 0.45;
Matches 46; Conservative 24; Mismatches 59; Indels 52; Gaps 10;

QY 6 MSTPLPAI-VPARKAT-----AAVIFLH-----GLDGTGVPRVPTLNNVAMPSPF 51
DB 14 VATTALVSAAPGAAHADPCSDIAVFAFGTHQASGLGVAFYDSLTSOVGGRS-- 71
QY 52 DIIGL----SPSOEDESIGIKOAEENIKALIDQEVKNGIPSRILIGFSOG----- 99
DB 72 --IGYAVNYASDDYRASASNGSDASAHQRTVAS--CPRTRYLGGYSGATVIDLST 128
QY 100 -----GALSLYTALT--QOKLAGVTALSLFLPLRXS-----FPQGPV--GGA 138
DB 129 SAMPAPVADHVAVALGCEPSSGFSMLMGSGSLPTIGPLYSKTNILCAPDDPCTGGG 188
QY 139 N 139
DB 189 N 189

RESULT 12

US-09-791-171-56
; Sequence 56, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WEIDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739

Db 15 VHGGD-----PLLIMGLGYNLSMHWHTVPTLAKRFKVIYEDNKGCVGKSSKAEQPSISIE 69
Qy 69 QAENIKALIDQEVKNGIPSNRIILGHSQGGALSPLYALTTOQK-----AGVTA 119

```

;      LENGTH: 256
;      TYPE: PRT
;      ORGANISM: Bacillus
;

```

```

; TYPE: PRT
; ORGANISM: E
US-09-950-368-2

```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2003, 03:15:41 ; Search time 77 Seconds
(Without alignments)
259.688 Million cell updates/sec

Title: US-09-988-982-1

Perfect score: 1070

Sequence: 1 MCGNNMSTPLPAIVPARKA.....CQCEMDVKQFIDKLPLPID 208

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	422.5	39.5	333	2 T23324	hypothetical prote
2	399	37.3	247	2 T52511	related to lysopho
3	318.5	29.8	224	2 T39158	lysophospholipase
4	306	28.6	227	2 S64955	probable membrane
5	273.5	25.6	224	2 H82658	carboxylesterase X
6	248	23.2	215	2 A83163	probable carboxyle
7	245	22.9	218	2 J00277	carboxylesterase (
8	244	22.8	218	2 J00865	esterase A (EC 3.1
9	240.5	22.5	471	2 T04911	hypothetical prote
10	163.5	15.3	204	2 S75304	serine esterase -
11	145.5	13.6	207	2 S43880	esterase - Splru1
12	134	12.5	214	2 AB2195	serine esterase, p
13	128.5	12.0	243	2 D72098	lysophospholipase
14	126	11.8	241	2 G86524	probable lysophosp
15	124	11.3	161	2 C96568	hypothetical prote
16	120.5	11.3	305	2 T20470	hypothetical prote
17	119.5	11.2	126	2 D96518	protein T2E6.14 (1
18	116	10.8	304	2 D86998	probable secreted
19	115	10.7	304	2 C70982	probable lpgc prot
20	108	10.1	239	2 F81704	serine esterase, p
21	108	10.1	319	2 AB1334	hypothetical prote
22	105.5	9.9	204	2 F83921	hypothetical prote
23	105.5	9.9	243	2 C95908	hypothetical prote
24	100	9.3	335	2 T20465	hypothetical prote
25	98	9.2	416	2 D70347	cell division prote
26	95.5	8.9	395	2 F72424	hypothetical prote
27	93.5	8.7	200	2 G96550	hypothetical prote
28	93	8.7	378	2 T41456	probable phosphosi

30	92.5	8.6	240	2 G91045	hypothetical prote
31	92.5	8.6	240	2 C85890	hypothetical prote
32	91	8.5	197	2 G90055	conserved hypothet
33	90.5	8.5	240	2 H65022	hypothetical prote
34	89.5	8.4	219	2 A70734	probable cutinase
35	89.5	8.4	691	2 C72454	hypothetical prote
36	88.5	8.3	215	2 D71634	hypothetical prote
37	88.5	8.3	239	2 A71552	probable lysophosp
38	87.5	8.2	216	2 C97843	serine esterase ho
39	86	8.0	961	2 H86181	hypothetical prote
40	85	7.9	332	2 F96568	probable lipase, 2
41	84.5	7.9	308	2 H70852	probable lipr prot
42	84	7.9	197	2 A96568	hypothetical prote
43	83	7.9	705	1 C1C1H	calpain (EC 3.4.22
44	83	7.8	293	2 S77419	hypothetical prote
45	83	7.8	501	2 C72321	conserved hypothet

ALIGNMENTS

RESULT 1
T23324
hypothetical protein K04G2.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23324
R:Gardner, A.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19727
A:Accession: T23324
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-333 <MIL>
A:Cross-references: EMBL:Z75712; PIDN:CAB0042.1; GSPDB:GN00019; CESP:K04G2.5
A:Experimental source: clone K04G2
C:Genetics:
A:Gene: CESP:K04G2.5
A:Map position: 1
A:Insertions: 8/1; 54/1; 87/1; 165/2; 263/3; 318/3

Query Match 39.5%; Score 422.5; DB 2; Length 333;
Best local similarity 44.2%; Pred. No. 7, 4e-32;
Matches 95; Conservative 23; Mismatches 66; Indels 31; Gaps 5;

QY	11	PAIVPAARKATAAIFLHGLGDTG-----PVRYTLNNVAM	47
DB	119	PSIVSPRGEHKGTLIFLHGLGDMADAFKTEAKHDKIKFICPHSSRPVTLNNGRM	178

QY	48	PSMFDIIGSPDSQDEDSGKQAAENIKALIDQEVKNGIPSNRIILGFSOGALSLYTA	107
DB	179	PAWFDFLEGLDPNAQDEDEQGNKATQYVHOLIDAQVAAIGPASTIAVAGFSKMGALATVYG	238

QY	108	LTFQOKLAGVTAFLPLRXSPQGPICG--ANRDISLQCHGDGDDPLVPIFGSLAYE	165
DB	239	LTFQOKLAGVTAFLPLRXSPQGPICG--ANRDISLQCHGDGDDPLVPIFGSLAYE	165

QY	166	KKTLVNPANVTFKYEAGMHSSQCEMDVKQFT	200
DB	295	YIKKF-NP-KVELHTYRGMQHSCEMDVKVTF	327

RESULT 2
T52511
related to lysophospholipase [imported] - *Neurospora crassa*
N:Alternate names: protein B2J23.70
C:Species: *Neurospora crassa*
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C:Accession: T52511
R:Schulte, U.; Alim, V.; Hohensel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, September 2000
A:Reference number: Z26053
A:Accession: T52511

OY 166 KLEKLVNPNVTEKTEGMMHSSCOQEMMDVKOFIDKL 204
 DB 182 HLGK--RGVTVTQOEYR-MGEVLVPEIHDIGAMLERL 217

RESULT 9

hypoetical protein T10114.130 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
 C:Accession: T04911
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
 submitted to the Protein Sequence Database, April 1998
 A:Reference number: Z15389
 A:Accession: T04911
 A:Molecule type: DNA
 A:Residues: 1-471 <BEV>
 A:Cross-references: EMBL:AL021712
 A:Experimental source: cultivar Columbia; BAC clone T10114
 C:Genetics:

A:Map position: 4
 A:Introns: 50/1; 67/3; 109/1; 158/3; 194/3; 221/1; 335/1; 352/3; 394/1; 434/3
 A:Note: T10114.130

Query Match 22.5%; Score 240.5; DB 2; Length 471;
 Best local similarity 30.6%; Pred. No. 1.4e-14;
 Matches 70; Conservative 30; Mismatches 80; Indels 49; Gaps 7;

OY 20 ATAAVIFLHGLDGPV-----RPVTLNPNVAMPSPFDI- 53
 DB 2 ARFIFLHGLDGPANEPITQFKSELNAMLPSAPENPVCNNGAVRSWFDVP 61

OY 54 -IGLSPDSQDESGIKQANIKALIDQEVKNIPSNRIILGFSOGALSLYALTATG 112
 DB 62 ELPPKVGSPIDESSVLEAVANNVHAIIIDQETAEISTPENVFICGLSGGALTTLASVLYRK 121

OY 113 KLGAVTALSPFLPLRKS---PQGPFGCANR-----DISILQCHGCDPLVPLMG 160
 DB 122 TLGGANLGSWVPFTSIISQFE---EAKKYPHLCPLINFIILSHGDDMVLEFENG 177

OY 161 SLVEKIKTLVNPANT--FKYEGMMHSSCOQEMMDVKOFIDKLPI 207
 DB 178 QAALPLFK---EAGVCEFKAPVGLGHSINKEKYIESWIKRRLKDI 222

RESULT 10
 S75304
 serine esterase - Synechocystis sp. (strain PCC 6803)
 N:Alternate names: protein s111284
 C:Species: Synechocystis sp.

A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C:Accession: S75304
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yasuda
 DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 S.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S75304
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-204 <KAN>

A:Cross-references: EMBL:D90904; GB:AB001339; NID:g1652225; PIDN:BA17218.1; PID:g165229
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 15.3%; Score 163.5; DB 2; Length 204;
 Best local similarity 29.6%; Pred. No. 7.7e-08;
 Matches 63; Conservative 36; Mismatches 73; Indels 41; Gaps 12;

OY 9 PLPAIVPAKATPAVIFLHGLG---DTGVPVPVT-----LNMNVAMP-----S 49
 DB 11 PDPAVPT--DSSYLLVNLHGWGADARDLSDLPMLDLPYQWRVFNAPPTTHQIQGR 68

OY 50 WEDTIGLSPDSQDESGIKQANENKA-LIDQEVKNIPSNRIILGFSOGALSLYALT 108
 DB 69 WIDL-----ESQNEF-GLAQARQGLRATLGLAETGIPLARTILGFSOGAMALDVL 122

OY 109 TTQOKLAGVTALSPFLPLR-XSPGPIGKANRDISILQCHGCDPLVPLMFGSLVTEK 167
 DB 123 TLV--PLAKIFSLISGLYHFPQSPQPA-----IAPILHGTEDPVPVPLMAQAKAEL 173

OY 168 KLVNPNVTEKTEGMMHSSCOQEMMDVKOFI 200
 DB 174 ESI--GASVEYQEFV-MGHAIPLMALRLKSF 203

RESULT 11

S43880
 esterase - Spirulina platensis
 C:Species: Spirulina platensis
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999
 C:Accession: S43880
 R:Salvi, S.; Trinel, M.; Janfaloni, L.; Pon, C.L.
 Mol. Gen. Genet. 243, 124-126, 1994

A:Title: Cloning and characterization of the gene encoding an esterase from Spirulina
 A:Reference number: S43880; MUID:94247351; PMID:8190066
 A:Accession: S43880
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-207 <SAL>

A:Cross-references: GB:S70419; NID:g546788; PIDN:AAB30793.1; PID:g546789

Query Match 13.6%; Score 145.5; DB 2; Length 207;
 Best local similarity 29.8%; Pred. No. 3.8e-06;
 Matches 61; Conservative 26; Mismatches 75; Indels 43; Gaps 11;

OY 24 VIFLHGLG---DTGVPVTLNPNVAMP--WFDI-----IGLSPDSQDE 64
 DB 20 IIFLHGWGANCDELTFLEAPM---LRPNVFEFPEAPFPHPVPGGRANYALETQYE 74

OY 65 SGIKQANENKALIDQ---EVKNIPSNRIILGFSOGALSLYALTATGOKLAGVTAL 120
 DB 75 -GIESREK---LIDWLNALIAOTTGIPQRTILGFSOGAMTEDEVGT--MGRAGLIVL 128

OY 121 SPLPLRKSFPQGPFGCANRDISILQCHGCDPLVPLMFGSLVTEKTLVNPANVTFT 180
 DB 129 SCYLHFKPEPQOTPLP-----PLMANGKQDMVPLCAHAQARDSPQKL--GATVEYHE 180

OY 181 YEGMMHSSCOQEMMDVKOFIDKL 205
 DB 181 Y-NMGHEICPDILGLIOSEFVTKLP 204

RESULT 12

AB2195
 serine esterase [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AB2195
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriku
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AB2195
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-214 <KUN>
 A:Cross-references: GB:BA000019; PIDN:BA074812.1; PID:g17132207; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:

Query Match 12.5%; Score 134; DB 2; Length 214;

Tue Jan 21 10:18:28 2003

us-09-988-982-1.rpr

Page 6

QY 150 DCDPLVPIMGSLVEKLTLVNPNVTFEKTIEGMMHSCQQ 191
 : | : | : | : | :
Db 162 -----HPFHVPYLFEKRRLHCSCSE 181

Search completed: January 19, 2003, 03:24:47
Job time : 79 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2003, 02:36:55 ; Search time 78 Seconds
(without alignments)
110.604 Million cell updates/sec

Title: US-09-988-982-1

Perfect score: 1070
Sequence: 1 MCGNNMSTPLPAIVPARKA.....COOEMMDVKQFIDKLPPID 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	245	22.9	218	1	EST2_PSEFL
2	244	22.8	218	1	EST1_PSEFL
3	126	11.8	241	1	YE88_SCHPO
4	90.5	8.5	232	1	YFPH_ECOLI
5	89.5	8.4	219	1	CUT2_MYCTU
6	88.5	8.3	215	1	Y744_RICPR
7	84	7.9	252	1	CLCD_RHOOP
8	84	7.9	705	1	CANX_CHICK
9	83	7.8	501	1	Y890_THEMA
10	82	7.7	655	1	RRAL_CABEL
11	81.5	7.6	320	1	HEM3_SYNY3
12	81.5	7.6	358	1	LIP_PSEFL
13	80.5	7.5	271	1	EST2_PSEFL
14	80	7.5	370	1	ACOC_PSEPU
15	79.5	7.4	608	1	BDD_PSEAE
16	79	7.4	217	1	CUT1_MYCTU
17	79	7.4	247	1	CUT3_MYCTU
18	79	7.4	400	1	YIEL_ECOLI
19	78.5	7.3	275	1	PRXC_STRLI
20	78.5	7.3	284	1	BOHO_RHOCA
21	78.5	7.3	399	1	PKR_ANASP
22	78.5	7.3	749	1	PA24_HORSE
23	77.5	7.2	364	1	LIP_BURCE
24	77.5	7.2	969	1	MSU1_YEAST
25	77	7.2	247	1	YFBB_HAEIN
26	77	7.2	580	1	PROA_XANCP
27	76.5	7.1	245	1	HIS4_YERPE
28	76.5	7.1	449	1	HTRA_BACSU
29	76	7.1	263	1	PI7A_ORYSA
30	76	7.1	319	1	ABS_ECOLI
31	76	7.1	417	1	PGK_CANNA
32	76	7.1	429	1	HISX_METJA
33	76	7.1	954	1	BTRL_YEAST

34	76	7.1	1162	1	LEPR_RAT	O62959 rattus norv
35	75.5	7.1	364	1	LIP_PSESS	P25275 pseudomonas
36	75.5	7.1	754	1	MBPL_KLUTA	P39679 kluyveromyc
37	75.5	7.1	837	1	XINZ_CLOTH	P10478 clostridium
38	75.5	7.1	1081	1	CARB_RALSO	O8x283 ralstonia s
39	75	7.0	230	1	CUT1_FUSSC	O99174 fusarium so
40	75	7.0	414	1	PHAI_PSELE	P52090 pseudomonas
41	75	7.0	785	1	MUS2_BACSU	P94545 bacillus su
42	75	7.0	381	1	PCGV_BOVIN	P81282 bos taurus
43	74.5	7.0	235	1	BTRL_RAT	P55007 rattus norv
44	74.5	7.0	1275	1	COBN_PSEDE	P29929 pseudomonas
45	74	6.9	428	1	YE63_SCHPO	O14249 schizosacch

ALIGNMENTS

RESULT 1	EST2_PSEFL	STANDARD	PRT	218 AA
ID	EST2_PSEFL			
AC	Q53547			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Carboxylesterase 2 (EC 3.1.1.1) (Esterase II).			
GN	ESTB.			
OS	Pseudomonas fluorescens.			
OC	Bacteria: Proteobacteria; gamma subdivision; Pseudomonadaceae;			
OX	Pseudomonas.			
NCBI_Taxid=294;				
RP	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.			
RX	MEDLINE=92134742; PubMed=1368750.			
RA	Hong K.H., Jang W.H., Choi K.D., Yoo O.J.;			
RT	"Characterization of Pseudomonas fluorescens carboxylesterase:			
RT	cloning and expression of the esterase gene in Escherichia coli.;"			
RL	Agric. Biol. Chem. 55:2839-2845(1991).			
RN	(2)			
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).			
RX	MEDLINE=98104086; PubMed=9438866;			
RA	Kim K.K., Song H.K., Shin D.H., Hwang K.Y., Choe S., Yoo O.J.;			
RA	Suh S.W.;			
RT	"Crystal structure of carboxylesterase from Pseudomonas fluorescens,			
RT	an alpha/beta hydrolase with broad substrate specificity.;"			
RL	Structure 5.1571-1584(1997).			
CC	- FUNCTION: HYDROLASE CARBOXYLIC ESTER BONDS WITH RELATIVELY BROAD			
CC	SUBSTRATE SPECIFICITY.			
CC	- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a			
CC	carboxylic anion.			
CC	- SUBUNIT: HOMODIMER.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sid.ch).			
DR	EMBL: S79600; AAC60403.1; -			
DR	PDB: LAUO; 04-MAR-98.			
DR	PDB: LAUR; 04-MAR-98.			
DR	InterPro: IPR003140; PLP_Gesterase.			
DR	InterPro: IPR000379; Ser_estrs-site.			
DR	Pfam: PF02230; abhydrolase_2; 1.			
KW	Hydrolase; Serine esterase; 3D-structure.			
FT	ACT_SITE 114			
FT	ACT_SITE 168			
FT	ACT_SITE 199			
FT	SEQUENCE 218 AA; 23880 MW; 6FID4537410E4CB4 CRC64;			
Query Match	22.9%; Score 245; DB 1; Length 218;			
Best Local Similarity	33.0%; Pred. No. 1.9e-15;			

[illegible]

```

RESULT 2
ESTL_PSEFL
ID ESTL_PSEFL STANDARD: PRT: 218 AA.
AC Q51738;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Carboxylesterase 1 (EC 3.1.1.1) (Esterase 1).
GN ESTA.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxId=294;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu F.;
RL Submitted (AUG-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: HYDROLYZE CARBOXYLIC ESTER BONDS WITH RELATIVELY BROAD
CC SUBSTRATE SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D00852; BAA00727.1; -.
DR HSP: Q53547; 1AUO.
DR InterPro: IPR003140; PLP_Cesterase.
DR InterPro: IPR000379; Ser_estrs_sste.
DR Pfam: PF02230; abhydrolase_2; 1.
DR Hydrolase; Serine esterase.
FT ACT_SITE 114 114 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 168 168 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 199 199 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SSEQUENCE 218 AA; 24153 MW; B61AE76AFED6ED CRC64;
-----
Query Match 22.88; Score 244; DB 1; Length 218;
Best Local Similarity 32.08; Pred. No. 2.4e-15;
Matches 70; Conservative 31; Mismatches 88; Indels 30; Gaps 5;
QY 11 PAIVPAARKATAAVYIFHLGLG-----DTGVPVPTLNMNVA 46
| : : : : : |
Db 4 PLIIQPAKRPADACIWIHLGAGADRYDPLVPAALQETLLSTRVLPQAPRPVPIIINGYE 63
| : : : : : |
QY 47 MPSEWEDITIGLSPDSQEDSGIKQAENIKALIDQEVKNGIPSNRIILIGFSQGALSLEYT 106
| : : : : : |
Db 64 MPSEWYDIKAMSPARSISILEELETSAKTYVDLIETQGRGIDITSIFLAGFSQGAVYFHT 123
| : : : : : |
QY 107 ALTT-QQKLACGYALSLPLPLKRSFPQGPPIGAGNRDISIILQCHGDCDPLVPLMFGSLTVE 165
| : : : : : |

```

```

Db      124 AFKMEGELGVIALSTYAPTFPNDIDQ--LSASQQNIPPLICLHGQYDEVONAMGRSAYE 181
Oy      166 KLKLTVNPANTFTFYEGNMHSSCOQEMMDVQFIDIKLL 204
        ||| | | | | | | | | | | | | | | | | | | |
Db      182 HLKG--RGVITWQEYP-MGEVLVPQEHIDIGAMLAERL 217

RESULT 3
YE88_SCHPO STANDARD; PRT; 241 AA.
AC      014304;
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      15-JUN-1998 (Rel. 36, Last sequence update)
DE      Hypothetical protein C9G1.08c in chromosome I.
GN      SPAC9G1.08C.
OS      Schizosaccharomyces pombe (fission yeast).
OC      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC      Schizosaccharomycetales; Schizosaccharomycetaceae;
CX      NCBI_TaxID=4896;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=9712;
RX      MEDLINE=21848401; PubMed=11859360;
RA      Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA      Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA      Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA      Collins M., Connor R., Cronin A., Davis P., Feltyell T., Fraser A.,
RA      Gerltz S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA      Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA      James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,
RA      Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA      Oliver K., O'Neill S., Pearson D., Quail M.A., Rabdinowitsch E.,
RA      Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA      Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA      Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA      Woodward J., Volckaert G., Aert R., Robben J., Garrenprez B.,
RA      Wellens I., Vanstreels E., Rieger M., Schefer M., Mueller-Auer S.,
RA      Gabel C., Fuchs M., Fritz C., Holzner E., Moselt D., Hilbert H.,
RA      Borzym K., Langer I., Beck A., Lemrach H., Reinhardt R., Pohl T.M.,
RA      Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
RA      Goftau A., Cadieu E., Dreano S., Gloux S., Lelaune V., Motlier S.,
RA      Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA      Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA      Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA      Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA      Cerutti L., Lowe T., McCamble W.R., Paulsen I., Potashkin J.,
RA      Sipakovskii G.V., Ussery D., Barrett B.G., Nurse P.;
RL      "The genome sequence of Schizosaccharomyces pombe."
       Nature 415:871-880(2002).
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to licenses@isb-sib.ch).
CC      -----
DR      EMBL; Z98763; CAB11492.1; -
DR      InterPro; IPRO03140; PLP_Cestrase.
DR      InterPro; IPRO00379; Ser_estrse.site.
DR      Pfam; PF02230; abhydrolase_2; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 241 AA; 27341 MW; BEFGC2DIB7DBFE21 CRC64;

Query Match          11.8%; Score 126; DB 1; Length 241;
Best Local Similarity 20.7%; Pred. 0.0002;
Matches 46; Conservative 35; Mismatches 65; Indels 76; Gaps 7;

```

```

DB      2  SLSNVLSNACAEIIECKDKVHNVILMHGIDGSHSFMAMAKNVLPTNTSYLSGFPY 61
      37  RPTVLNNVAMP-----WFDIIGLSPDSQ--EDESCIQAQENIKALIDQEVKNCIPSNRI 91
      62  R---LPLDFENPDGNNMGEDVHFDQNGELQSEADFSKFSFMIINLGNLISGILSSRI 118
      92  ILGGSOGGALSLYTA--LTTQOKLAGVTALSLPLRLXSPQPIGANDISILQCHG 149
      DB      119  FFFGGGAGMVALYSCYKLSYKYLQGLGIFSGGTLPLSTLPN----- 161
      150  DDDPLVLMFGSLTYEKLTVNPANVTFKYEKGMMHSCCOO 191
      DB      162  -----HPPHVVYLFKRIKHCSCSE 181

```

RESULT 4
YPFH_ECOLI

```

ID      YPFH_ECOLI      STANDARD:      PRT:      232 AA.
AC      P76561.
DT      01-NOV-1997 (Rel. 35, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical protein ypfh.
GN      ypfh OR B2473.
OS      Escherichia coli.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Escherichia.
OX      NCBI_TaxID=562;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=K12 / MG1655;
RX      MEDLINE=9742617; PubMed=9278503;
RA      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA      Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA      Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA      Mau B., Shao Y.;
RT      "The complete genome sequence of Escherichia coli K-12.";
RL      Science 277:1453-1474(1997).
CC      -1- SIMILARITY: TO R.PROMAELKII RP744.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AE000334; AAC75526.1; ALT_INIT.
DR      EcoGene: EG14195; ypfh.
DR      InterPro: IPR003140; PLP_Cesterase.
DR      InterPro: IPR000379; Ser_ester_1.
DR      Pfam: PF02230; abhydrolase_2; 1.
KM      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 232 AA; 24855 MW; E046F9D642076B41 CMC64;

```

Query Match 8.5%; Score 90.5; DB 1; Length 232;
Best Local Similarity 22.1%; Pred. NO. 0.35;
Matches 49; Conservative 39; Mismatches 83; Indels 51; Gaps 10;

```

QY      18  RKATAAVIEFHGLGDT-----GPRVPTLNMNV--AMPS-----WFDIIGLS 57
      13  KPAQQLLLFHGVDNPPVAMGETGMWFAFLPFDALVAVSGAEPGSGNAGROMFSVQGIT 72.
      58  PDSOEDSEGIKQAE-----IKALIDQEVKNCIPSNRIILGFSOGGALSLYTALTQTQ 111
      DB      73  EN-----RQARVDALIMPTETIVRWQKSGVGANATALIGFSQ--GAIIVLESIKAE 124
      QY      112  QKLAGVTALSLPLRLXSPQPIGANDISILQCHGDDPLVLMFGSLTYEKLTV 171
      DB      125  PGIA-----SRVIAFNGRVASLP-ETASTATTIHLHGGEDEVIDLAAHVAQAQAL--IS 176

```

```

QY      172  NPANVTFKYEKGMMHSSCOEEMDV-----KOFIDKL 204
      DB      177  AGGDVTLIDIVEDLGHAIIDNRSMQFALDHLRYTIPKHFPEAL 218

```

RESULT 5
CUT2_MYCTU

```

ID      CUT2_MYCTU      STANDARD:      PRT:      219 AA.
AC      O50664.
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Probable cutinase RV2301 precursor (EC 3.1.1.74).
GN      RV2301 OR MT2358 OR MTCY339.08C.
OS      Mycobacterium tuberculosis.
OC      Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC      Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX      NCBI_TaxID=1773;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=H37Rv;
RX      MEDLINE=98295987; PubMed=9634230;
RA      Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA      Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA      Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA      Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
RA      Hornsby T., Jagels K., Kroh A., McLean J., Moule S., Murphy L.,
RA      Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA      Rutter S., Seeger K., Skelton S., Squares S., Squares K.,
RA      Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT      "Deciphering the biology of Mycobacterium tuberculosis from the
RT      complete genome sequence.";
RL      Nature 393:537-544(1998).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CDC 1551 / Oshkosh;
RA      Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA      Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA      Kolonay J.F., Nelson W.C., Umayam L.A., Ertolavea M.D., Salzberg S.L.,
RA      Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA      Bishai W.;
RT      "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT      laboratory strains.";
RL      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC      -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC      -1- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: Z77163; CAB00997.1; -.
DR      EMBL: AE007078; AKK46643.1; -.
DR      HSSP: P00590; ICEX.
DR      TIGR: MT2358; -.
DR      TubercuList: RV2301; -.
DR      InterPro: IPR000675; Cutinase.
DR      Pfam: PF01083; Cutinase; 1.
DR      PROSITE: PS00155; CUTINASE_1; 1.
DR      PROSITE: PS00931; CUTINASE_2; FALSE_NEC.
KM      Hypothetical protein; Hydrolase; Serine esterase; Signal;
KW      Complete proteome.
FT      SIGNAL 1 33
FT      CHAIN 34 219
FT      DISULFID 34 181
FT      DISULFID 101 174
FT      DISULFID 112 172
FT      ACT_SITE 178 178
FT      ACT_SITE 178 178
FT      ACT_SITE BY SIMILARITY.
FT      ACT_SITE BY SIMILARITY.
FT      ACT_SITE BY SIMILARITY.

```


CC Thermotogaceae; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of Thermotoga maritima";
 RL Nature 399:323-329(1999).
 CC -1- COFACTOR: Zinc (Probable).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (By similarity).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M50B.
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AE001754; MADS5971.1; -
 CC DR TIGR: TM0890; -
 CC DR InterPro: IPR001478; PDZ.
 CC DR InterPro: IPR000130; Zn_MTPeptidase.
 CC DR Pfam: PF00595; PDZ; 1.
 CC DR SMART: SM00226; PDZ; 1.
 CC DR PROSITE: PS50106; PDZ; 1.
 CC DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 CC DR Hypothetical protein; Hydrolase; Metalloprotease; Zinc; Transmembrane;
 CC Inner membrane; Complete proteome.
 CC KW METAL: 17 17 ZINC (CATALYTIC) (POTENTIAL).
 CC FT ACT_SITE 18 18 ZINC (CATALYTIC) (POTENTIAL).
 CC FT METAL 21 21 ZINC (CATALYTIC) (POTENTIAL).
 CC FT TRANSMEM 93 115 POTENTIAL.
 CC FT TRANSMEM 401 420 POTENTIAL.
 CC FT TRANSMEM 427 449 POTENTIAL.
 CC FT TRANSMEM 474 496 POTENTIAL.
 CC FT DOMAIN 96 180 PDZ.
 CC SQ SEQUENCE 501 AA; 55875 MW; CE3E58117DC2A9A CRC64;
 Query Match 7.8%; Score 83; DB 1; Length 501;
 Best Local Similarity 25.8%; Pred. No. 4.3;
 Matches 31; Conservative 24; Mismatches 43; Indels 22; Gaps 7;
 OY 38 PVTLMNVMVPSWFDIIGSPDSQEDSESGIKQA-----AENIK-----ALIDQEVKNGIRS 88
 DB 113 PVTLMNVMVPSWFDIIGSPDSQEDSESGIKQA-----AENIK-----ALIDQEVKNGIRS 169
 OY 89 NRILIGSGGALSITATLTQOKLAGVTALSFLLPKRSFPGQPI--GGANRDISIIO 146
 DB 170 ELVTI--RNGEKSL--RLTPMY--PETYEVLSEADGIPSGKLVYNGNRDTSYK 221
 RESULT 10
 RFAL CAEEL
 ID RFAL CAEEL STANDARD; PRT; 655 AA.
 AC 019537;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Probable replication factor A 73 kDa subunit (RP-A) (RF-A)
 DE (Replication factor-A protein 1).
 DE F18A1.5.
 GN Caenorhabditis elegans.
 OS

CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX Kistner J.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS TO SINGLE-STRANDED SEQUENCES (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: TO OTHER SPECIES RFAL/RFAL.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U41535; AAB63407.1; -
 CC DR HSSP: P27694; LJC.
 CC DR WormPep: F18A1.5; CE04405.
 CC DR InterPro: IPR004591; Rpal.
 CC DR InterPro: IPR004365; tRNA_antl.
 CC DR Pfam: PF01336; tRNA_antl; 2.
 CC DR TIGRFAMs: TIGR00617; rpal; 1.
 CC KW DNA replication; DNA-binding; Zinc-finger; Nuclear protein.
 CC ZN_FING 518 539
 CC SQ SEQUENCE 655 AA; 73202 MW; 44E41E7B16E2FB42 CRC64;
 Query Match 7.7%; Score 82; DB 1; Length 655;
 Best Local Similarity 26.9%; Pred. No. 7.4;
 Matches 42; Conservative 19; Mismatches 57; Indels 38; Gaps 8;
 OY 63 DESG-----IKQAMENIKALIDQEVKNGIPSNRII---LGSFGGALSITATLTQOK 113
 DB 387 DESGALVRLTLMGDEATLADVDYQKVIARFVGPREFNGFSLGTGSA--FTIISVPE 444
 OY 114 LAGVAL-----SFLPLPKRSFPGQPIGGAN--RDISILOCHDDCPPLVPMFGS---- 161
 DB 445 IAGVELDWYANAKPTTEVKMMSQAGSGSEAPRTTIGLO-----EMQGRKSDK 495
 OY 162 --LVEKIKTLVNPANVTFTYEGMMSQCOEEM 194
 DB 496 GDYATVKAMITRVNPTNA--LYRGCASEGCGKTLV 528
 RESULT 11
 HEM3--SYNY3
 ID HEM3--SYNY3 STANDARD; PRT; 320 AA.
 AC P73660;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Porphobilinogen deaminase (EC 4.3.1.8) (PBG) (Hydroxymethylblane
 DE synthase) (HMB) (Pre-uroporphyrinogen synthase).
 DE HEMC OR SLR1887.
 GN Synecocystis sp. (strain PCC 6803).
 OS Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA MiyaJima N., Hiroseawa M., Sugiyama M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K.,
 RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";

RL DNA Res. 3:109-136(1996).
 CC -1- FUNCTION: TETRAPOLYMERIZATION OF THE MONOPYRROLE PBG INTO THE
 CC HYDROXYMETHYLBILANE PREDOPORPHYRINOGEN IN SEVERAL DISCRETE STEPS.
 CC -1- CATALYTIC ACTIVITY: 4 porphobilinogen + H(2)O =
 CC hydroxymethylbilane + 4 NH(3).
 CC -1- COFACTOR: COVALENTLY BINDS A DIPHYROMETHANE COFACTOR TO WHICH
 CC THE PORPHOBILINOGEN SUBUNITS ARE ADDED.
 CC -1- PATHWAY: Porphyrin biosynthesis by the C5 pathway; fourth step.
 CC Involved in chlorophyll biosynthesis.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HMBs FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D90908; BAA17705.1; -.
 DR HSP; P06983; IPDA.
 DR InterPro; IPR000860; Porphobil_deam.
 DR Pfam; PF01379; Porphobil_deam; 1.
 DR PRINTS; PR00151; PORPHBDMNASE.
 DR ProDom; PD002745; Porphobil_deam; 1.
 DR TrEMBL; TIGR00212; henc; 1.
 DR PROSITE; PS00533; PORPHOBILINOGEN_DEAM; 1.
 DR Porphyrin biosynthesis; Chlorophyll biosynthesis; Lyase;
 KM Complete proteome.
 FT BINDING 249 249 PYRROMETHANE COFACTOR (BY SIMILARITY).
 SQ SEQUENCE 320 AA; 34894 MW; 6A3C9CAF81CA183 CRC64;
 Query Match 7.6%; Score 81.5; DB 1; Length 320;
 Best Local Similarity 21.2%; Pred. No. 3.4;
 Matches 48; Conservative 40; Mismatches 81; Indels 57; Gaps 8;
 QY 6 MSTPLAIVPARKATAVIFLHGLGDPYRPVTLMMNVAMPSPDILGSPDSODES 65
 Db 3 VSTSPYVRISSKSSQALVOTYVQF-----ELQKHPFPRQDVE 43
 QY 66 GIKQAENI-----KALIDQEVKNGIPNRILLGSGGALSTYALTQCKLA 115
 Db 44 TMEQGGKILDLVALAKIGDKGLFTQELJEDGMLKRTDLAVHS---LKDLPNLPAGMLG 100
 QY 116 GVT-----ALSFLLPLR-----XSPFGPFGGAN--RDSIILOCHDCDPLVPLMGSL 162
 Db 101 CVTRKVPADALVILNARKQKDLASLPEGAVIGTSSLRLLQLRYH-----FPHL 150
 QY 163 IVEKIKTLVNP--ANVTFKTEGMMHSSCOEEMDVAKQFIDKLLP 206
 Db 151 TFKVGRGVNTRLAKLDSNEYDAITLLAAGLERLDMANRIDQLIP 196
 RESULT 12
 LIP_PSEGL STANDARD; PRT; 358 AA.
 AC 005489;
 ID LIP_PSEGL
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
 GN LIPA.
 OS Pseudomonas glumae, and
 OS Chromobacterium viscosum.
 OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
 OC Burkholderia.
 OX NCBI_TaxID=337, 42739;
 RN [1]
 RP SEQUENCE FROM N.A.: SEQUENCE OF 40-61, AND MUTAGENESIS.
 RC SPECIES-P. glumae; STRAIN-PGI / CBS 322.89;
 RX MEDLINE=93119130; PubMed=1476423;
 RA Frenken L.G.J., Egmond M.R., Batenburg A.M., Bos J.W., Visser C.,

RA Verrips C.T.;
 RT "Cloning of the Pseudomonas glumae lipase gene and determination of
 RT the active site residues."; Appl. Environ. Microbiol. 58:3787-3791(1992).
 RL [2]
 RN SEQUENCE OF 40-54, AND CHARACTERIZATION.
 RP SPECIES-C. viscosum;
 RC MEDLINE=95306500; PubMed=7786905;
 RX Taipa M.A., Liebeton K., Costa J.V., Cabral J.M.S., Jaeger K.-E.;
 RT Lipase from Chromobacterium viscosum: biochemical characterization
 RT indicating homology to the lipase from Pseudomonas glumae.;
 RL Biochim. Biophys. Acta 1256:396-402(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RC SPECIES-P. glumae; PubMed=8405390;
 RX MEDLINE=94009622; PubMed=8405390;
 RA Noble M.E.M., Cleasby A., Johnson L.N., Egmond M.R., Frenken L.G.J.;
 RT "The crystal structure of triacylglycerol lipase from Pseudomonas
 RT glumae reveals a partially redundant catalytic aspartate.";
 RL FEBS Lett. 331:123-128(1993).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RC SPECIES-C. viscosum; STRAIN-ATCC 6918;
 RX MEDLINE=96275656; PubMed=8683577;
 RA Lang D., Hofmann B., Haalick L., Hecht H.-J., Spener F., Schmid R.D.,
 RA Schomburg D.;
 RT "Crystal structure of a bacterial lipase from Chromobacterium
 RT viscosum ATCC 6918 refined at 1.6-A resolution.";
 RL J. Mol. Biol. 259:704-717(1996).
 CC -1- FUNCTION: HYDROLYSIS OF TRIGLYCERIDES.
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -1- COFACTOR: REQUIRES CALCIUM.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
 CC LIPASE FAMILY.
 CC -----
 CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X70354; CAA49812.1; -.
 DR EMBL; A16323; CAA01279.1; -.
 DR EMBL; A32021; CAA02073.1; -.
 DR PIR; A48952; A48952.
 DR PIR; S37291; S37291.
 DR PDB; 1TAH; 31-MAY-94.
 DR InterPro; IPR000073; Abhydrolase.
 DR InterPro; IPR000734; Lipase.
 DR InterPro; IPR000379; Serests_site.
 DR Pfam; PF00561; abhydrolase; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Hydrolyase; Lipid degradation; Signal; Calcium; 3D-structure.
 FT SIGNAL 1 39
 FT CHAIN 40 358
 FT ACT_SITE 126 126
 FT ACT_SITE 302 302
 FT ACT_SITE 324 324
 FT ACT_SITE 324 324
 FT DISULFID 229 308
 FT MUTAGEN 54 54
 FT MUTAGEN 126 126
 FT MUTAGEN 160 160
 FT MUTAGEN 160 160
 FT MUTAGEN 160 160
 FT MUTAGEN 280 280
 FT MUTAGEN 280 280
 FT MUTAGEN 302 302
 FT MUTAGEN 302 302
 H->A: NO LOSS OF ACTIVITY.
 S->A: COMPLETE LOSS OF ACTIVITY.
 D->E: NO LOSS OF ACTIVITY.
 D->A: NO LOSS OF ACTIVITY.
 D->E: NO LOSS OF ACTIVITY.
 D->A: COMPLETE LOSS OF ACTIVITY.
 D->E: NO LOSS OF ACTIVITY.
 D->A: 75% LOSS OF ACTIVITY.

FT MUTAGEN 324 324 H->A: COMPLETE LOSS OF ACTIVITY.
 FT CONFLICT 40 40 A->W (IN REF. 2).
 SQ SEQUENCE 358 AA: 36928 MW: FE7B5D7A22EC6B4B CRC64:

Query Match
 Best Local Similarity 27.0%; Pred. No. 3.9;
 Matches 34; Conservative 13; Mismatches 52; Indels 27; Gaps 5;

QY 11 PAIVPAKAKATA--AVIFHIGLDTGPRVPTLNNVAMPSEFDILGSPDSQ----- 61
 DB 35 PAAVADTYAATRRYPVLVHGLAGIDKEFANV-----VDIY-----GIQSDIQSHGAKVY 84
 QY 62 -----EDESIGKQAEVNIKALIDQEVNKGIPSNRIILGFSOGGALSLYTALTTOOKL 114
 DB 85 VANLSFGQSDGPNRGEDLLAVKQ-VLAATGATKVNLIHSGGGLNSRYVAAPQV 143
 QY 115 AGVTAL 120
 DB 144 ASVTTI 149

RESULT 13
 ESTE_PSEFL STANDARD: PRT: 271 AA.

ID AC P22862;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Arylesterase (EC 3.1.1.2) (Aryl-ester hydrolase).
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SIK WI;
 RC MEDLINE=95219101; PubMed=7704276;
 RA Pelletier I., Altenbucher J.;
 RT "A bacterial esterase is homologous with non-haem haloperoxidases and
 displays brominating activity.";
 RT Microbiology 141:459-468(1995).
 RN [2]
 RP PRELIMINARY SEQUENCE FROM N.A., AND SEQUENCE OF 1-17.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U12537; AAB60168.1; -
 CC EMBL: D12484; BAA02052.1; ALT_FRAME.
 CC PIR: J00606; J00606.
 CC DR HSSP: O31158; IAS8.
 CC DR InterPro: IPR000073; Abhydrolase.
 CC DR InterPro: IPR000379; Ser_estr_site.
 CC DR Pfam: PF00561; abhydrolase; 1.
 CC KM Hydrolase.
 CC FT INT_MET 0 0 BY SIMILARITY.
 CC FT ACT_SITE 94 94

FT ACT_SITE 222 222 BY SIMILARITY.
 FT ACT_SITE 251 251 BY SIMILARITY.
 SQ SEQUENCE 271 AA: 29961 MW: 1ADA219AD8130123 CRC64;

Query Match
 Best Local Similarity 19.5%; Pred. No. 3.5;
 Matches 41; Conservative 23; Mismatches 57; Indels 89; Gaps 8;

QY 71 AENIKALIDQEVNKGIPSNRIILGFSOGGA-LSLYTALTTOOKLAGVTALSFLLP--- 126
 DB 73 ADDIAQLIEH-----LDLKEVTLVGFSGMGDDVARIARHGSARVAGVLGAVTPLFGQ 127
 QY 127 RXSEPGQ-----PIGAGR----- 140
 DB 128 KPDYQGVPLDVFAFRTTELLKDRAGFLSDFNAPFYGINKGVSQGVOTQIALLAS 187
 QY 141 -----DISTLQCHGDDPLVPL-MGSLTVERKTLVNPANV 176
 DB 188 LKATVDCVTAFETDFRPDMAKIDVPTLVHGDSDQIVPEFTGKVAELIK-----GA 241
 QY 177 TFKTYEGMMH-----SSCOEMMDVKQFIDK 202
 DB 242 ELKYTKAPRPGFATVTHAQQLMEDLLAFIKR 271

RESULT 14
 ACOC_PSEPU STANDARD: PRT: 370 AA.

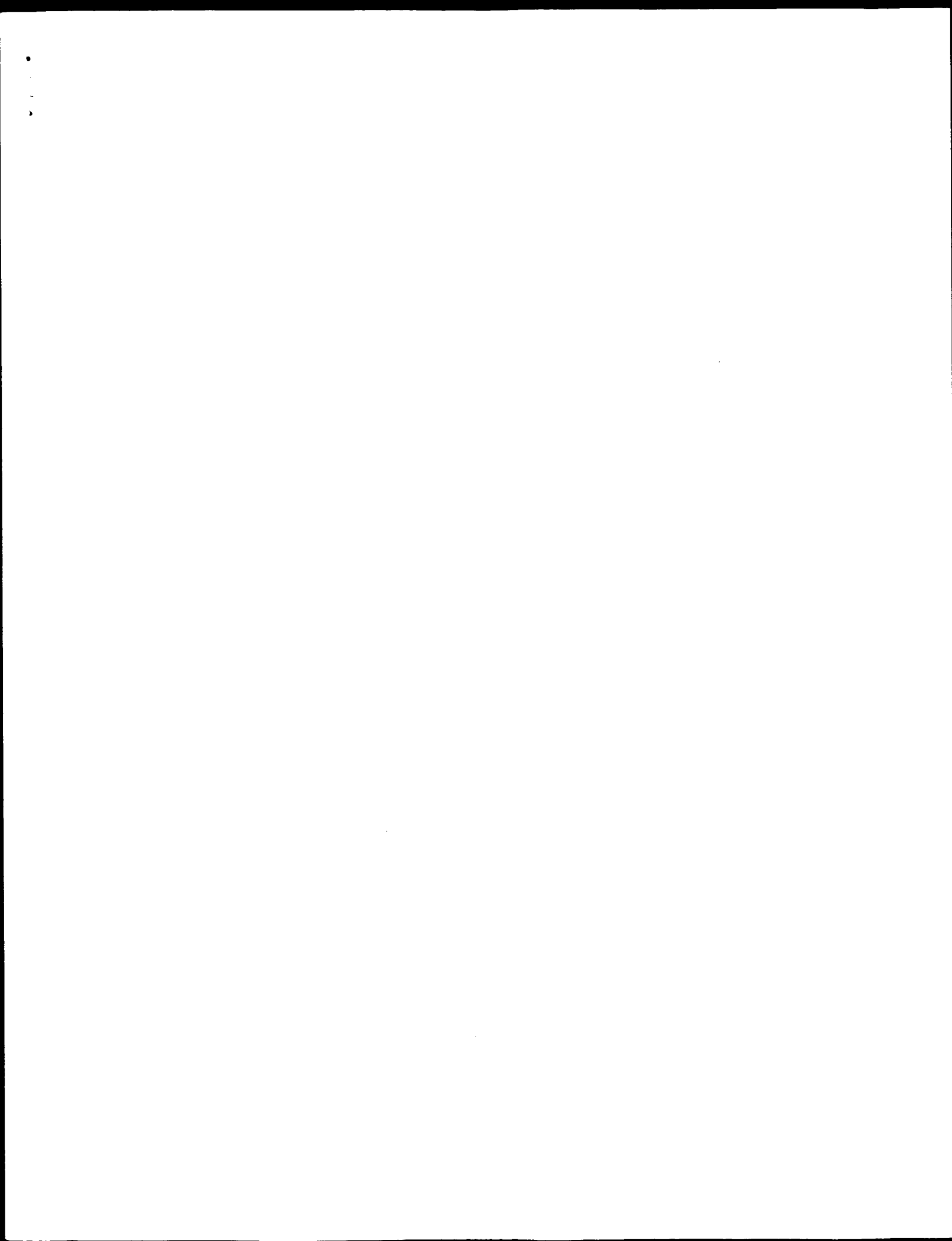
ID ACOC_PSEPU
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dihydrolipoamide acetyltransferase component of acetoacetyl
 DE system (EC 2.3.1.12) (Acetoacetyl dehydrogenase E2 component).
 DE ACOC.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.

CC STRAIN-PRG2;
 CC MEDLINE=95113288; PubMed=7813883;
 CC Huang M., Oppermann F.B., Steinbuechel A.;
 CC "Molecular characterization of the Pseudomonas putida 2,3-butanediol
 CC catabolic pathway.";
 CC FEBS Microbiol. Lett. 124:141-150(1994).
 CC
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide -> CoA + S-
 CC acetylhydrolipoamide.
 CC -1- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
 CC -1- PATHWAY: Acetoacetyl catabolism.
 CC -1- SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: L35343; AAB58981.1; -
 CC HSSP: P10515; IFYC.
 CC DR InterPro: IPR003089; AB_hydrolase.
 CC DR InterPro: IPR000073; Abhydrolase.
 CC DR InterPro: IPR000089; Biotin_lipoyl.
 CC DR InterPro: IPR003016; Lipoyl.
 CC DR InterPro: IPR000379; Ser_estr_site.
 CC DR Pfam: PF00364; biotin_lipoyl; 1.
 CC DR Pfam: PF00561; abhydrolase; 1.
 CC DR PRINTS: PR00111; ABHYDROLASE.
 CC DR PROSITE: PS00189; LIPOYL; 1.

CC This SWI2-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

Search completed: January 19, 2003, 03:21:31
Job time : 100 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2003, 03:14:05 ; Search time 112 Seconds
(without alignments)
382.659 Million cell updates/sec

Title: US-09-988-982-1
Perfect score: 1070
Sequence: 1 MCGNNMSTPLPAIVAPARRA.....COQEMMDVKQFIDKLPPID 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1034	96.6	230	4	075608
2	968	90.5	230	6	077821
3	968	90.5	230	11	P97823
4	958	89.5	230	11	P70470
5	949	88.7	214	4	Q9UQF9
6	935	87.4	219	6	077820
7	723	67.6	231	11	Q9QYL8
8	717	67.0	231	11	Q9QYL7
9	713	66.6	231	4	Q9S372
10	672	62.8	231	4	Q9UGEO
11	499	46.6	104	4	Q43202
12	490	45.8	216	5	Q917R0
13	422.5	39.5	223	5	Q21224
14	406.5	38.0	227	5	Q9U8F2
15	406.5	38.0	229	5	Q18501
16	397	37.1	245	3	Q9HFJ5

17	318.5	29.8	224	3	042881	042881 schizosacch
18	306	28.6	227	3	Q12354	Q12354 saccharomyc
19	273.5	25.6	224	16	Q9PCY0	Q9PCY0 xyliella fas
20	265	24.8	235	5	Q9YGV9	Q9YGV9 drosophila
21	248	23.2	215	16	Q9HXE7	Q9HXE7 pseudomonas
22	240.5	22.5	471	10	Q49635	Q49635 arabidopsis
23	238	22.2	239	11	Q8R065	Q8R065 mus musculu
24	227.5	21.3	237	4	Q96AV0	Q96AV0 homo sapien
25	209.5	19.6	257	10	Q94E46	Q94E46 oryza sativ
26	205.5	19.2	255	10	Q91W14	Q91W14 arabidopsis
27	172	16.1	195	10	Q9SSS4	Q9SSS4 arabidopsis
28	163.5	15.3	204	16	P73192	P73192 synecocyst
29	145.5	13.6	207	2	Q53415	Q53415 spirulina p
30	134	12.5	214	16	Q8YSH2	Q8YSH2 anabaena sp
31	128.5	12.0	243	16	Q9ZMR7	Q9ZMR7 chlamydia p
32	124	11.6	161	10	Q9SSS3	Q9SSS3 arabidopsis
33	120.5	11.3	200	10	Q9FT37	Q9FT37 oryza sativ
34	120.5	11.3	305	5	Q9XVAT	Q9XVAT caenorhabdi
35	119.5	11.2	126	10	Q9FZP5	Q9FZP5 arabidopsis
36	116	10.8	302	2	Q49658	Q49658 mycobacteri
37	116	10.8	304	16	Q9CCU5	Q9CCU5 mycobacteri
38	115	10.7	304	16	P96903	P96903 mycobacteri
39	108	10.1	239	16	Q9PKQ2	Q9PKQ2 chlamydia m
40	108	10.1	319	16	Q8Y518	Q8Y518 listeria mo
41	105.5	9.9	204	16	Q9KAW2	Q9KAW2 bacillus ha
42	105.5	9.9	243	16	Q92W16	Q92W16 rhizobium m
43	100.5	9.4	344	16	Q8XYT6	Q8XYT6 raltsonia s
44	100	9.3	300	16	Q8XDM2	Q8XDM2 raltsonia s
45	100	9.3	335	5	Q9XVB2	Q9XVB2 caenorhabdi

ALIGNMENTS

RESULT 1
ID 075608 PRELIMINARY; PRT; 230 AA.
AC 075608;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Lysophospholipase (Acyl-protein thioesterase-1) (lysophospholipase DE 1).
GN LPL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hu G.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shen Y., Guan Z., Gu J., Ye M., Zhou J., Zhang Q., Xu S., He K.,
RA Shen S., Mao M., Chen Z.;
RT *Human lysophospholipase gene*;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA PubMed=11080636;
RT Dedejiev Y., Dauter Z., Kuznetsov S.R., Jones T.L., Derewenda Z.S.;
RT *Crystal structure of the Human Acyl Protein Thioesterase I from a RT Single X-Ray Data Set to 1.5 A.*;
RL Structure 8:1137-1146(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA TISSUE=BONE MARROW;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE;

RA Strausberg R.;
 RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF081281; AAC31610.1; -
 DR EMBL: AF077198; AAD26993.1; -
 DR EMBL: AF291053; AAG10063.1; -
 DR EMBL: BC010397; AAH10397.1; -
 DR EMBL: BC008652; AAH08652.1; -
 DR HSSP: 053547; IAUO.
 DR PMAA-2DPAGE; 075608; -
 DR InterPro: IPR003140; PLP_Cesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF02230; abhydrolase_2; 1.
 SQ SEQUENCE 230 AA; 24669 MW; 90C0522F765FIAC6 CRC64;

Query Match 96.6%; Score 1034; DB 4; Length 230;
 Best Local Similarity 89.1%; Pred. No. 1.2e-92;
 Matches 205; Conservative 0; Mismatches 3; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPAARAKATAVIFLHGLDGTG-----PVRP 38
 DB 1 MCGNNMSTPLPAIVPAARAKATAVIFLHGLDGTGMAEAFAGIRSHIKYICPHAPVR 60
 QY 39 VTLNNMAMPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 DB 61 VTLNNMAMPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGLSLVLTALTTQOKLAGVYALSFLLPRKSPGPIGGANDISILQCHGCDPLVPLM 158
 DB 121 GGLSLVLTALTTQOKLAGVYALSFLLPRKSPGPIGGANDISILQCHGCDPLVPLM 180
 QY 159 FGSITVEKLTIVNPANVTERTYEGMHSSCOQEMMDVKQFIDKLLPID 208
 DB 181 FGSITVEKLTIVNPANVTERTYEGMHSSCOQEMMDVKQFIDKLLPID 230

RESULT 2

077821 PRELIMINARY; PRT; 230 AA.
 AC 077821;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Calcium-independent phospholipase A2 isoform 2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=98308497; PubMed=9644627;
 RA Porfilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dal G.,
 RA Sasser M., Cheng J., Buonanno A.;
 RT "CDNA cloning and expression of a novel family of enzymes with
 RT calcium-independent phospholipase A2 and lysophospholipase
 RT activities.";
 RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
 DR EMBL: U97148; AAC63432.1; -
 DR HSSP: 053547; IAUO.
 DR InterPro: IPR002106; AATRNA_ligaseII.
 DR InterPro: IPR003140; PLP_Cesterase.
 DR Pfam: PF02230; abhydrolase_2; 1.
 DR PROSITE: PS00339; AA_TRNA_LIGASE II 2; UNKNOWN 1.
 SQ SEQUENCE 230 AA; 24687 MW; 89AF2017AEFC9FAC CRC64;

Query Match 90.5%; Score 968; DB 6; Length 230;
 Best Local Similarity 81.7%; Pred. No. 3.1e-86;
 Matches 188; Conservative 8; Mismatches 12; Indels 22; Gaps 1;

QY 1 MCGNNMSTPLPAIVPAARAKATAVIFLHGLDGTG-----PVRP 38
 DB 1 MCGNNMSTPLPAIVPAARAKATAVIFLHGLDGTGMAEAFAGIRSHIKYICPHAPVR 60

QY 39 VTLNNMAMPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 98
 DB 61 VTLNNMAMPWFDDIIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGGFSQ 120
 QY 99 GGLSLVLTALTTQOKLAGVYALSFLLPRKSPGPIGGANDISILQCHGCDPLVPLM 158
 DB 121 GGLSLVLTALTTQOKLAGVYALSFLLPRKSPGPIGGANDISILQCHGCDPLVPLM 180
 QY 159 FGSITVEKLTIVNPANVTERTYEGMHSSCOQEMMDVKQFIDKLLPID 208
 DB 181 FGSITVEKLTIVNPANVTERTYEGMHSSCOQEMMDVKQFIDKLLPID 230

RESULT 3

077823 PRELIMINARY; PRT; 230 AA.
 AC 077823;
 DT 01-MAY-1997 (TREMblrel. 03, Created)
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE LPHOSPHOLIPASE 1A (EC 3.1.1.5) (lysophospholipase I) (LECITHINASE B)
 DE (LYSOLECITHINASE) (phospholipase B) (adult male kidney CDNA, RIKEN
 DE FULL-length enriched LIBRARY, clone:0610025N20, FULL INSERT sequence)
 DE (lysophospholipase I).
 GN LYP1A1 OR PLA1A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang A., Deems R.A., Dennis E.A.;
 RL J. Biol. Chem. 0:0-0(0).
 RN [2]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kaota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleishmann W., Gaasterland T., Gissi C., Kling B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
 RA Blake J., Botfield D., Boujunga N., Carrincci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshniew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
 CC GLYCEROPHOSPHOCHOLINE + A FATTY ACID ANION.
 DR EMBL: U89352; AAB4627.1; -
 DR EMBL: AK002674; BAB22276.1; -
 DR EMBL: BC013536; AAH13536.1; -
 DR HSSP: 053547; IAUO.
 DR MGD: MGI:1344588; Lyp1a1.
 DR InterPro: IPR002106; AATRNA_ligaseII.
 DR InterPro: IPR003140; PLP_Cesterase.
 DR InterPro: IPR000379; Ser_estrs_site.

DR Pfam: PF02230; abhydrolase.2; 1.
DR PROSITE: PS00339; AA_TRNA_LIGASE_IL_2; UNKNOWN.1.
KW Hydrolase.
SQ SEQUENCE 230 AA; 24687 MW; 89AF2017AEFC9FAC CRC64;

Query Match 90.5%; Score 968; DB 11; Length 230;
Best Local Similarity 81.7%; Pred. No. 3,1e-86;
Matches 188; Conservative 8; Mismatches 12; Indels 22; Gaps 1;

OY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTG-----PVRP 38
DB 1 MCGNNMSAPMPAVPAARKATAVIFLHGLDGTGAGAEAFAGIKSPIHIKTCPHAPVMP 60
OY 39 VTLNNNVAMPSPWFDITIGLSPDSQDESGIKQAENIKALIDQEVKNIGPSNRITLLGFSQ 98
DB 61 VTLNNNVAMPSPWFDITIGLSPDSQDESGIKQAETVKALIDQEVKNIGPSNRITLLGFSQ 120
OY 99 GGALSLYLTALTTQOKLAGVTALSCWLPRLASFSGQPIINSANRDISVLQCHGDCDPLVPLM 158
DB 121 GGALSLYLTALTTQOKLAGVTALSCWLPRLASFSGQPIINSANRDISVLQCHGDCDPLVPLM 180
OY 159 FGSLLVEKILKTLVNPANVTFTKTEGMMHSSCOQEMDMVKOFIDKLLPPID 208
DB 181 FGSLLVEKILKTLVNPANVTFTKTEGMMHSSCOQEMDMVKOFIDKLLPPID 230

RESULT 4

P70470 PRELIMINARY; PRT; 230 AA.

AC P70470:
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE LYSOPHOSPHOLIPASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=LIVER;
RX MEDLINE=96205961; PubMed=8631810;
RA Sugimoto H., Hayashi H., Yamashita S.;
RT "Purification, cDNA cloning, and regulation of lysophospholipase from rat liver."
RL J. Biol. Chem. 271:7705-7711(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOPHALAMUS;
RX MEDLINE=98308497; PubMed=9644627;
RA Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G.,
RA Saener M., Cheng J., Buonanno A.;
RT "cDNA cloning and expression of a novel family of enzymes with calcium-independent phospholipase A2 and lysophospholipase activities."
RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
DR EMBL: D63885; BAA09935.1; -;
DR EMBL: U97146; AAC63430.1; -;
DR HSSP: Q53547; 1A00.
DR InterPro: IPR002106; AATRNA_LigaseII.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR000379; Ser_estr_site.
DR Pfam: PF02230; abhydrolase.2; 1.
DR PROSITE: PS00339; AA_TRNA_LIGASE_IL_2; UNKNOWN.1.
SQ SEQUENCE 230 AA; 24709 MW; AAFB8C4702EAD74 CRC64;

Query Match 89.5%; Score 958; DB 11; Length 230;
Best Local Similarity 81.7%; Pred. No. 2,9e-85;
Matches 188; Conservative 7; Mismatches 13; Indels 22; Gaps 1;

OY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTG-----PVRP 38
DB 1 MCGNNMSAPMPAVPAARKATAVIFLHGLDGTGAGAEAFAGIKSPIHIKTCPHAPVMP 60

OY 39 VTLNNNVAMPSPWFDITIGLSPDSQDESGIKQAENIKALIDQEVKNIGPSNRITLLGFSQ 98
DB 61 VTLNNNVAMPSPWFDITIGLSPDSQDESGIKQAETVKALIDQEVKNIGPSNRITLLGFSQ 120
OY 99 GGALSLYLTALTTQOKLAGVTALSCWLPRLASFSGQPIINSANRDISVLQCHGDCDPLVPLM 158
DB 121 GGALSLYLTALTTQOKLAGVTALSCWLPRLASFSGQPIINSANRDISVLQCHGDCDPLVPLM 180
OY 159 FGSLLVEKILKTLVNPANVTFTKTEGMMHSSCOQEMDMVKOFIDKLLPPID 208
DB 181 FGSLLVEKILKTLVNPANVTFTKTEGMMHSSCOQEMDMVKOFIDKLLPPID 230

RESULT 5

O9UOF9 PRELIMINARY; PRT; 214 AA.

ID O9UOF9:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Lysophospholipase isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2049367; PubMed=11042152;
RA Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,
RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells."
RL Genome Res. 10:1546-1560(2000).
DR EMBL: AF077199; AAD26994.1; -;
DR HSSP: Q53547; 1A00.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR000379; Ser_estr_site.
DR Pfam: PF02230; abhydrolase.2; 1.
SQ SEQUENCE 214 AA; 22875 MW; 63BCC806F509CE8 CRC64;

Query Match 88.7%; Score 949; DB 4; Length 214;
Best Local Similarity 88.4%; Pred. No. 2e-84;
Matches 191; Conservative 4; Mismatches 11; Indels 10; Gaps 2;

OY 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTG-----PVRPVTLMNVAMPSPWFD 52
DB 1 MCGNNMSTPLPAIVPAARKATAVIFLHGLDGTGAGAEAFAGIR--SHIKTCCHAD 58
OY 53 IIGLSPDSQDESGIKQAENIKALIDQEVKNIGPSNRITLLGFSOGALSTYLTALTTQO 112
DB 59 IIGLSPDSQDESGIKQAENIKALIDQEVKNIGPSNRITLLGFSOGALSTYLTALTTQO 118
OY 113 KLAGVTALSTLPLRXSPGPIGAGNRDISVLQCHGDCDPLVPLMFGSLTYEKLTVN 172
DB 119 KLAGVTALSTLPLRXSPGPIGAGNRDISVLQCHGDCDPLVPLMFGSLTYEKLTVN 178
OY 173 PANVTFTKTEGMMHSSCOQEMDMVKOFIDKLLPPID 208
DB 179 PANVTFTKTEGMMHSSCOQEMDMVKOFIDKLLPPID 214

RESULT 6

O77820 PRELIMINARY; PRT; 219 AA.

ID O77820:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calcium-independent phospholipase A2 isoform 1 (Fragment).
OS Oryctolagus cuniculus (Rabbit).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=98308497; PubMed=9644627;
RA Portella D., Crew M.D., Grant A., Serrero G., Bates L.M., Dai G.,
  Sasser M., Cheng J., Buonanno A.;
RT "cDNA cloning and expression of a novel family of enzymes with
  calcium-independent phospholipase A2 and lysophospholipase
  activities."
RL J. Am. Soc. Nephrol. 9:1178-1186(1998).
DR EMBL: U97147; AAC63431.1; -.
DR HSSP: Q53547; IAUO.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF02230; abhydrolase_2; 1.
FT NON_TER
SQ SEQUENCE 219 AA; 23602 MW; 3B6A4FEDC3BC912B CRC64;

Query Match 87.4%; Score 935; DB 6; Length 219;
Best Local Similarity 85.4%; Pred. No. 4,8e-83;
Matches 187; Conservative 2; Mismatches 8; Indels 22; Gaps 1;

OY 12 AIVPARKKATAAIVFLHGLDGTG-----PVRPTLNNVAMP 49
DB 1 ASVPAARKKATAAIVFLHGLDGTGHCWAEEAFGRSHIYICPHAFVMTLNNMAMS 60
OY 50 WPDIIIGSPDSDESGIKOAEENIKALIDOEYKNGIPSNRIILGSGGALSLYTALT 109
DB 61 WPDIIIGSPDSDESGIKOAEENIKALIDOEYKNGIPSNRIILGSGGALSLYTALT 120
OY 110 TQOKLAGVRLSLFLRLKRSFPGGPIGCGANRDISIIQCHGDCDPLVPLFGSITVEKLT 169
DB 121 TQOKLAEVRLSLFLRLKRSFPGGPIGCGANRDISIIQCHGDCDPLVPLFGSITVEKLT 180
OY 170 LVNPANVTFTYEGMMHSSCOCEMMOVKOFIDKLPPID 208
DB 181 LVNPANVTFTYEGMMHSSCOCEMMOVKOFIDKLPPID 219

RESULT 7
O9QYTL8 PRELIMINARY; PRT; 231 AA.
AC O9QYTL8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Lysophospholipase II.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC Sugimoto H.;
RT "Rat lysophospholipase II."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB021645; BAA87911.1; -.
DR HSSP: Q53547; IAUO.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF02230; abhydrolase_2; 1.
SQ SEQUENCE 231 AA; 24807 MW; 49A710C5A997C7C1 CRC64;

Query Match 67.6%; Score 723; DB 11; Length 231;
Best Local Similarity 61.6%; Pred. No. 2.4e-62;
Matches 143; Conservative 27; Mismatches 36; Indels 26; Gaps 3;

OY 1 MCGNNMSTPL---PAIVPARKKATAAIVFLHGLDGTG-----P 35
DB 1 MCGNNMSTPL---PAIVPARKKATAAIVFLHGLDGTGHSWADALSTIRLPHVYICPHAF 60

```

```

OY 36 VRPVTLNNVAMPSPFMDIIGSPDSDESGIKOAEENIKALIDOEYKNGIPSNRIILG 95
DB 61 RIVPTLNNKVMPSFMDIIGSPDSDESGIKOAEENIKALIDOEYKNGIPSNRIILG 120
OY 96 FSGGALSLEYALTTOOKLAGVRLSLFLRLKRSFPGGPIGCGANRDISIIQCHGDCDPLV 155
DB 121 FSGGALSLEYALTTOOKLAGVRLSLFLRLKRSFPGGPIGCGANRDISIIQCHGDCDPLV 179
OY 156 PLMGSLTVEKLTLVNPANVTFTYEGMMHSSCOCEMMOVKOFIDKLPPID 207
DB 180 PVRFGALTAERLRTVYVPAFQVFTYEGMMHSSCOCEMMOVKOFIDKLPPV 231

RESULT 8
O9QYTL7 PRELIMINARY; PRT; 231 AA.
AC O9QYTL7;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Lysophospholipase II (Lysophospholipase 2).
GN LYP1A2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=99165589; PubMed=10064901;
RA Toyoda T., Sugimoto H., Yamashita S.;
RT "Sequence, expression in Escherichia coli, and characterization of
  Lysophospholipase II."
RL Biochim. Biophys. Acta 1437:182-193(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata Y., Yoshino M., Itoh M., Ishii Y.,
  Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
  Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
  Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
  Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
  Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
  Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
  Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
  Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
  Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
  Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
  Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
  Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AB009653; BAA6751.1; -.
DR EMBL: AK003689; BAB22940.1; -.
DR HSSP: Q53547; IAUO.
DR MGD: MGI:1347000; Lyp1a2.
DR InterPro: IPR003140; PLP_Cestrase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF02230; abhydrolase_2; 1.
SQ SEQUENCE 231 AA; 24794 MW; E18797A17570AA97 CRC64;

Query Match 67.0%; Score 717; DB 11; Length 231;
Best Local Similarity 61.2%; Pred. No. 9.1e-62;
Matches 142; Conservative 27; Mismatches 37; Indels 26; Gaps 3;

OY 1 MCGNNMSTPL---PAIVPARKKATAAIVFLHGLDGTG-----P 35

```

```

Db 1 MCGNTMSVPLLTDAATVSGAERTAAVIFLHGLDGTGSHMADALSTRPHVKYICHPAP 60
Qy 36 VRPVTLMNNVAMPSPWFIDIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGG 95
Db 61 RLPVTLNKKVMPSWFDLMGISPDAPEDEAGIKKAENIKALIEHEMKNGIPANRIYVLGG 120
Qy 96 FSOGGALSIVTALTQOKLAGVTALSFLLPLRKSPGPGPIGGANRDISILQCHGDCDPLV 155
Db 121 FSOGGALSIVTALTQOKLAGVTALSFLLPLRKSPGPGPIGGANRDISILQCHGDCDPLV 179
Qy 156 PLMFSGSLTVEKTKTLVNPANVTFTYEGSMHSSCOQEMMDVKOPIDKLPPV 207
Db 180 PVRFGALTAELKRSVTPARVQFRTYGVHSSCPQEMAAVKEFLKLPV 231

RESULT 9
ID 095372 PRELIMINARY; PRT; 231 AA.
AC 095372:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Acyl-protein thioesterase (Lysophospholipase II).
GN D386K2.4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Kuznetsov S.R., Jones T.L.Z.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Frankland J.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA; AND COLON;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098668; AAC72844.1; -
DR EMBL; AL031295; CAB40158.1; -
DR EMBL; BC017193; AAH17193.1; -
DR EMBL; BC017034; AAH17034.1; -
DR HSSP; Q33547; IAUO.
DR InterPro; IPR003140; PIP_Cesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF02230; abhydrolase_2; 1.
SQ SEQUENCE 231 AA; 24737 MW; 813C9C71757C5135 CRC64;

Query Match 66.6%; Score 713; DB 4; Length 231;
Best Local Similarity 60.8%; Pred. No. 2.2e-61;
Matches 141; Conservative 28; Mismatches 37; Indels 26; Gaps 3;

Qy 1 MCGNNMSTPL---PAIVPAARKATAAVIFLHGLDGTG-----P 35
Db 1 MCGNTMSVPLLTDAATVSGAERTAAVIFLHGLDGTGSHMADALSTRPHVKYICHPAP 60
Qy 36 VRPVTLMNNVAMPSPWFIDIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGG 95
Db 61 RLPVTLNKKVMPSWFDLMGISPDAPEDEAGIKKAENIKALIEHEMKNGIPANRIYVLGG 120
Qy 96 FSOGGALSIVTALTQOKLAGVTALSFLLPLRKSPGPGPIGGANRDISILQCHGDCDPLV 155
Db 121 FSOGGALSIVTALTQOKLAGVTALSFLLPLRKSPGPGPIGGANRDISILQCHGDCDPLV 179
Qy 156 PLMFSGSLTVEKTKTLVNPANVTFTYEGSMHSSCOQEMMDVKOPIDKLPPV 207
Db 180 PVRFGALTAELKRSVTPARVQFRTYGVHSSCPQEMAAVKEFLKLPV 231

```

```

RESULT 10
ID 09060 PRELIMINARY; PRT; 231 AA.
AC 09060:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE D570F3.6 (novel protein similar to lysophospholipase II (LYPLA2)).
GN D570F3.6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mashreghi-Mohammadi M.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF050332; CAB63783.1; -
DR HSSP; Q33547; IAUO.
DR InterPro; IPR003140; PIP_Cesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF02230; abhydrolase_2; 1.
SQ SEQUENCE 231 AA; 24985 MW; 0C12C486013DBE8A CRC64;

Query Match 62.8%; Score 672; DB 4; Length 231;
Best Local Similarity 58.2%; Pred. No. 2.2e-57;
Matches 135; Conservative 29; Mismatches 42; Indels 26; Gaps 3;

Qy 1 MCGNNMSTPL---PAIVPAARKATAAVIFLHGLDGTG-----P 35
Db 1 MCGNTMSVPLLTDAATVSGAERTAAVIFLHGLDGTGSHMADALSTRPHVKYICHPAP 60
Qy 36 VRPVTLMNNVAMPSPWFIDIGLSPDSQDESGIKQAENIKALIDQEVKNGIPSNRIILGG 95
Db 61 RLPVTLNKKVMPSWFDLMGISPDAPEDEAGIKKAENIKALIEHEMKNGIPANRIYVLGG 120
Qy 96 FSOGGALSIVTALTQOKLAGVTALSFLLPLRKSPGPGPIGGANRDISILQCHGDCDPLV 155
Db 121 FSOGGALSIVTALTQOKLAGVTALSFLLPLRKSPGPGPIGGANRDISILQCHGDCDPLV 179
Qy 156 PLMFSGSLTVEKTKTLVNPANVTFTYEGSMHSSCOQEMMDVKOPIDKLPPV 207
Db 180 PVRFGALTAELKRSVTPARVQFRTYGVHSSCPQEMAAVKEFLKLPV 231

RESULT 11
ID 043202 PRELIMINARY; PRT; 104 AA.
AC 043202:
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Probable lysophospholipase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRN;
RA MEDLINE-96207227; PubMed=8619474;
RA Andersson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;
RT "A double adaptor" method for improved shotgun library
RT construction";
RL Anal. Biochem. 236:107-113(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRN;
RA MEDLINE-97264341; PubMed=9110174;
RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;

```

"Large-scale concatenation cdna sequencing.";
 RL Genome Res. 7:353-358(1997).
 DR EMBL: AF035293; AAB8180.1; -;
 DR InterPro: IPR003140; PLP_Cesterase.
 DR Pfam: PF02230; abhydrolase_2; 1.
 FT NON_TER
 SQ SEQUENCE 104 AA; 11403 MW; CB6C320EBA1011B3 CRC64;
 Query Match 46.6%; Score 499; DB 4; Length 104;
 Best Local Similarity 97.0%; Pred. No. 5,4e-41;
 Matches 96; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 110 TQOKLAGVTALSFLLPLRXSPFGPGIGGANDRISILGCHGDDPLVPLMGSLTYEKLKT 169
 DB 6 TQOKLAGVTALSCWLPRLRASFPQIGGANDRISILGCHGDDPLVPLMGSLTYEKLKT 65
 QY 170 LVNPANVTFTKTEYGMHSSCOEDMDVKOFIDKLPLPD 208
 DB 66 LVNPANVTFTKTEYGMHSSCOEDMDVKOFIDKLPLPD 104
 RESULT 12
 Q917R0 PRELIMINARY; PRT; 216 AA.
 AC Q917R0;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CG18815 protein (GH04560p).
 GN CG18815.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abriil J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borzova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Honick J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J.V., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svikas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STAPLETON-BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guart H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celinker S.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO03544; AAC22322.1; -;
 DR EMBL: AY094672; AAM11025.1; -;
 DR HSSP: Q53547; 1AUO.
 DR FLYBase: FBgn0042138; CG18815.
 DR InterPro: IPR003140; PLP_Cesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF02230; abhydrolase_2; 1.
 SQ SEQUENCE 216 AA; 23162 MW; 4566B9E0148AB7CB CRC64;
 Query Match 45.8%; Score 490; DB 5; Length 216;
 Best Local Similarity 48.1%; Pred. No. 1.1e-39;
 Matches 103; Conservative 24; Mismatches 61; Indels 26; Gaps 3;
 QY 11 PAIYPAARKATPAATVIFLHGLDTS-----PVRPVTINMNVAMP 48
 DB 4 PVIYEAIVKQTATITIFMHGLDITGHGSSSALAAIRPFPMKVICPTAPQVSLNAGFRMP 63
 QY 49 SWFDIIGLSPDSQDESGIKQAEINIKALIDQEVKNCIPSNRIILGFSOGGALSITVAL 108
 DB 64 SWFDLKLTDICGPDEPGICGARDVSHGMIQKETSAGIPANRIYLGFSOGGALATYSAL 123
 QY 109 TQOKLAGVTALSFLLPLRXSPFGPGIGGANDRISILGCHGDDPLVPLMGSLTYEKLKT 168
 DB 124 TYDQPLAGVVALSCWLPRLHOKFPGAKVN--SDVPITQAHGDDVPVYKFGQLSLSLK 181
 QY 169 TLVNPANVTFTKTEYGMHSSCOEDMDVKOFIDK 202
 DB 182 SFMK--NVTFTKTEYGLSHSSDDEMDVKIDISK 213
 RESULT 13
 Q21224 PRELIMINARY; PRT; 223 AA.
 ID Q21224;
 AC Q21224;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE K04G2.5 protein.
 GN K04G2.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdittida; Rhabdittolidae;
 OC Rhabdittidae; Pelodierinae; Caenorhabditts.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Gardner A.E.;
 RA submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99069613; PubMed=9851916;
 RX none;
 RA "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: Z75712; CAB00042.2; -;
 DR InterPro: IPR003140; PLP_Cesterase.
 DR InterPro: IPR000379; Ser_estrs_site.
 DR Pfam: PF02230; abhydrolase_2; 1.
 SQ SEQUENCE 223 AA; 24334 MW; 305C376F0D30E10 CRC64;

Query Match 39.5%; Score 422.5; DB 5; Length 223;
 Best Local Similarity 44.2%; Pred. No. 4,4e-33;
 Matches 95; Conservative 23; Mismatches 66; Indels 31; Gaps 5;

QY 11 PAIVPAAR-KATAVAVIFLHGLDGTG-----PVRPTLNMNVA 47
 DB 9 PSIVSPRGEHKGTLFLHGLDGTGHWADAFKTEAKHDNIKFIOPHSERPVTLNMGMRM 68
 QY 48 PSMFDIIGLSPDSQDEDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGGALSLYTA 107
 DB 69 PAMFDLGLDPAQDEDEGINRATQYVQLIDAEVAAIPASRIVAGSGMGALAIYAG 128
 QY 108 LTTQOKLAGVTAFLSLPLRXSPFOGPIG--ANRDISILQCHGDCDPLVPLMGSLTYE 165
 DB 129 LFTYQKLGIVGLSFLQRTKFP-----GSTANNATPIFLGHGTDFLVPLOFGQMSQ 184
 QY 166 KLKTLVNPANVTFTYEGMMHSSCOQEMMDVKOFI 200
 DB 185 YIKKF-NP-KVELHTYRGMSGSGEEMRDVKTFL 217

RESULT 14

ID Q908F2 PRELIMINARY; PRT; 227 AA.
 AC Q908F2;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Lysophospholipase.
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PHILIPPINE;
 RA Fan J., Brindley P.J.;
 RT "Cloning and overexpression in Escherichia coli and immunological
 assay of a lysophospholipase homolog from Schistosoma japonicum."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF091539; AAD52700.1; -;
 DR InterPro: IPR000923; BlueCu.1.
 DR InterPro: IPR003140; PLP_Cesterase.
 DR InterPro: IPR000379; Ser-estrs_site.
 DR Pfam: PF02230; abhydrolase_2; 1.
 DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.
 SQ SEQUENCE 227 AA; 24843 MW; FE3050D50B0A753 CRC64;

Query Match 38.0%; Score 406.5; DB 5; Length 227;
 Best Local Similarity 40.5%; Pred. No. 1.6e-31;
 Matches 89; Conservative 36; Mismatches 70; Indels 25; Gaps 5;

QY 10 LPAIVPAAR-KATAVAVIFLHGLDGTG-----PVRPTLNMNVA 46
 DB 6 LPAIVVASRSKHTATLFLHGLDGTGHWSDTLQVYVNYFKVICPHANSIPVTLNGMC 65
 QY 47 MPMFDIIGLSPDSQDEDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGGALSLYT 106
 DB 66 MPAMYDIFALSENKODEPGIKGASVELGKFAKIRAGIPVENIYIGFSGGSAVPLYN 125
 QY 107 ALTTQOKLAGVTAFLSLPLRXSPFOGPIG--IGANRDISILQCHGDCDPLVPLMGSLTYE 165
 DB 126 ALTSTLQYGGVAFSCWPLRHKFMSSPTLLTPKDVPIFOCHGLDCCMLPFAMGKLTHE 185
 QY 166 KLKTLVNPANVTFTYEGMMHSSCOQEMMDVKOFIDKLP 205
 DB 186 LKKNF-QLSKCELKCYPDLSHSCCEMEDLRFILARNIP 224

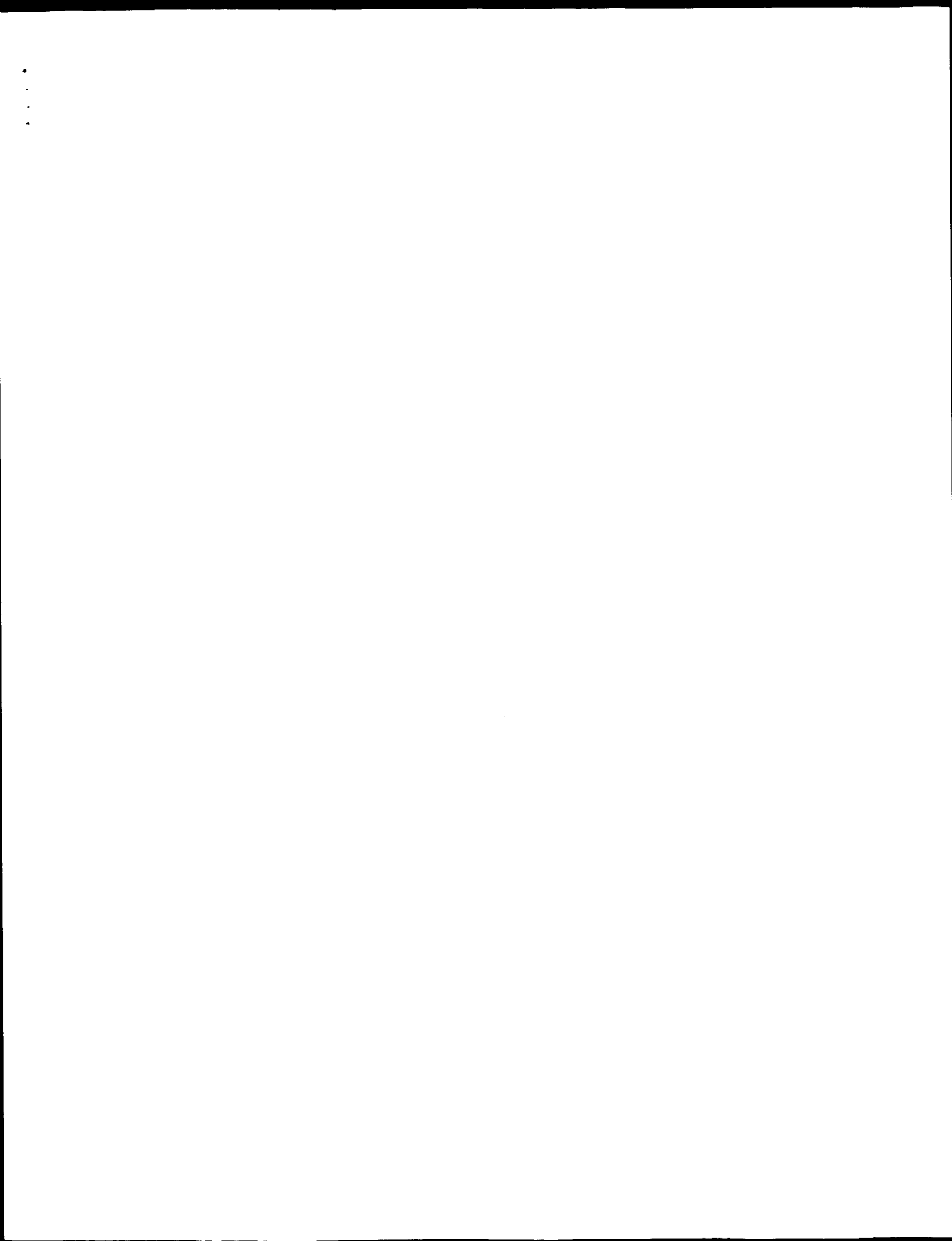
RESULT 15
 ID 018501 PRELIMINARY; PRT; 239 AA.

AC 018501;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JUN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Lysophospholipase homolog.
 GN SMLPLH.
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGYPTIAN;
 RX MEDLINE=99011094; PubMed=9797070;
 RA Hamdan F.F., Ribeiro P.;
 RT "Cloning and sequence analysis of a lysophospholipase homologue from
 Schistosoma mansoni."
 RL Parasitol. Res. 84:839-842(1998).
 DR EMBL; AF066678; AAC62254.1; -;
 DR InterPro: IPR000923; BlueCu.1.
 DR InterPro: IPR003140; PLP_Cesterase.
 DR InterPro: IPR000379; Ser-estrs_site.
 DR Pfam: PF02230; abhydrolase_2; 1.
 DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.
 SQ SEQUENCE 239 AA; 25870 MW; 8289D6563DC2D441 CRC64;

Query Match 38.0%; Score 406.5; DB 5; Length 239;
 Best Local Similarity 40.0%; Pred. No. 1.7e-31;
 Matches 88; Conservative 37; Mismatches 70; Indels 25; Gaps 4;

QY 10 LPAIVPAAR-KATAVAVIFLHGLDGTG-----PVRPTLNMNVA 46
 DB 18 LPAIVVASRSKHTATLFLHGLDGTGHWSDTLQVYVNYFKVICPHANSIPVTLNGMC 77
 QY 47 MPMFDIIGLSPDSQDEDESGIKQAENIKALIDQEVKNGIPSNRIILGFSOGGALSLYT 106
 DB 78 MPAMYDIFALSENKODEPGIKGASVELGKFAKIRAGIPVENIYIGFSGGSAVPLYN 137
 QY 107 ALTTQOKLAGVTAFLSLPLRXSPFOGPIG--IGANRDISILQCHGDCDPLVPLMGSLTYE 165
 DB 138 ALTSTLQYGGVAFSCWPLRHKFMSSPTLLTPKDVPIFOCHGLDXYIPFAMGKLTHE 197
 QY 166 KLKTLVNPANVTFTYEGMMHSSCOQEMMDVKOFIDKLP 205
 DB 198 LKTF-QLSKCELKCYPDLSHSCCEKEMGDLRTFLSKNIP 236

Search completed: January 19, 2003, 03:23:35
 Job time : 133 secs



score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Description

AR028701 Se

AR104346 Se

AX018183 Se

AR079197 Se

AR203099 Se

AR203084 Se

AT 365267 HI

BC010397 HQ

1107147 Oryz

1197146 Rat

BC013536 N

AR203091 5e

U89352 Mus musculus
AR203102 Sequence
AX341122 Sequence
AC116241 Rattus no
AC127539 Rattus no
AC111839 Rattus no
AC099137 Rattus no
AC118121 Rattus no
AC073054 Homo sapi
AF035293 Homo sapi
AC102108 Mus muscu
AB021645 Rattus no
BC017193 Homo sapi
BC017034 Homo sapi
AL113046 Sequence
AF096668 Homo sapi
AB096653 Mus muscu
AC040962 Homo sapi
AL050333 Human DNA
AL665821 Human DNA
AL667799 Human DNA
AC128713 Rattus no

source 1..709
/organism="unknown"
BASE COUNT 166 a 169 c 175 g 197 t 2 others
ORIGIN

Query Match 99.8%; Score 707.6; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 4e-176;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGACAGCCCTTGGGCGCGCGCGCGCTTCTTCCGCTTGGCGTGTG 60
DB 1 GCGGCTGACAGCCCTTGGGCGCGCGCGCGCTTCTTCCGCTTGGCGTGTG 60
QY 61 AGGTGAGGCGGTATGTGGGCAATTAACATGCAACCCCGCTGCCGCATGTGCGCG 120
DB 61 AGGTGAGGCGGTATGTGGGCAATTAACATGCAACCCCGCTGCCGCATGTGCGCG 120
QY 121 CCGCCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGGATTGGAGATACTGGGCTG 180
DB 121 CCGCCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGGATTGGAGATACTGGGCTG 180
QY 181 TTAGGCGCTTACATTAATATGAAGTGGCTATGCTTCAATGCTTGAATATATGGGC 240
DB 181 TTAGGCGCTTACATTAATATGAAGTGGCTATGCTTCAATGCTTGAATATATGGGC 240
QY 241 TTTCACAGATTCAAGAGAGATGAATCTGGATTAAACAGCAGCAGAAATATATAAG 300
DB 241 TTTCACAGATTCAAGAGAGATGAATCTGGATTAAACAGCAGCAGAAATATATAAG 300
QY 301 CTTTGATTTGATCAAGAAGTGAAGATGCAATCTTCTTAACAGAAATTTTGGAGGGT 360
DB 301 CTTTGATTTGATCAAGAAGTGAAGATGCAATCTTCTTAACAGAAATTTTGGAGGGT 360
QY 361 TTTCACAGGAGAGCTTATCTTTATATCTGCTTACACAGCAGCAAACTGGCAG 420
DB 361 TTTCACAGGAGAGCTTATCTTTATATCTGCTTACACAGCAGCAAACTGGCAG 420
QY 421 GTGTCACTGACAGCTTCTTCTTCCACTTGGGNTTCTTCCACAGGKCTATCG 480
DB 421 GTGTCACTGACAGCTTCTTCTTCCACTTGGGNTTCTTCCACAGGKCTATCG 480
QY 481 GTGTGCTAATATAGATATTTCTATCTCAGTGCACAGGGGATTTGACCTTTGGTTC 540
DB 481 GTGTGCTAATATAGATATTTCTATCTCAGTGCACAGGGGATTTGACCTTTGGTTC 540
QY 541 CCTGATGTTGGTCTCTTACGGTGGAAAACTAAACATTTGGATTCAGCCCAATG 600
DB 541 CCTGATGTTGGTCTCTTACGGTGGAAAACTAAACATTTGGATTCAGCCCAATG 600
QY 601 TGACCTTTAAACCTATGAAGATATGACAGATCTGTCTCAACAGGAATGATGATG 660
DB 601 TGACCTTTAAACCTATGAAGATATGACAGATCTGTCTCAACAGGAATGATGATG 660
QY 661 TCAAGCAATTCATTTGATTAACCTCTACCTTCAATTTGATTTGACGTACTA 709
DB 661 TCAAGCAATTCATTTGATTAACCTCTACCTTCAATTTGATTTGACGTACTA 709

RESULT 2
AR079196 709 bp DNA linear PAT 31-AUG-2000
LOCUS AR079196
DEFINITION Sequence 2 from patent US 5965423.
ACCESSION AR079196
VERSION AR079196.1 GI:10005942
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 709)
AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
TITLE Human lysophospholipase
JOURNAL Patent: US 5965423-A 2 12-OCT-1999;
FEATURES Location/Qualifiers

source 1..709
/organism="unknown"
BASE COUNT 166 a 169 c 175 g 197 t 2 others
ORIGIN

Query Match 99.8%; Score 707.6; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 4e-176;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGACAGCCCTTGGGCGCGCGCGCGCTTCTTCCGCTTGGCGTGTG 60
DB 1 GCGGCTGACAGCCCTTGGGCGCGCGCGCGCTTCTTCCGCTTGGCGTGTG 60
QY 61 AGGTGAGGCGGTATGTGGGCAATTAACATGCAACCCCGCTGCCGCATGTGCGCG 120
DB 61 AGGTGAGGCGGTATGTGGGCAATTAACATGCAACCCCGCTGCCGCATGTGCGCG 120
QY 121 CCGCCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGGATTGGAGATACTGGGCTG 180
DB 121 CCGCCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGGATTGGAGATACTGGGCTG 180
QY 181 TTAGGCGCTTACATTAATATGAAGTGGCTATGCTTCAATGCTTGAATATATGGGC 240
DB 181 TTAGGCGCTTACATTAATATGAAGTGGCTATGCTTCAATGCTTGAATATATGGGC 240
QY 241 TTTCACAGATTCAAGAGAGATGAATCTGGATTAAACAGCAGCAGAAATATATAAG 300
DB 241 TTTCACAGATTCAAGAGAGATGAATCTGGATTAAACAGCAGCAGAAATATATAAG 300
QY 301 CTTTGATTTGATCAAGAAGTGAAGATGCAATCTTCTTAACAGAAATTTTGGAGGGT 360
DB 301 CTTTGATTTGATCAAGAAGTGAAGATGCAATCTTCTTAACAGAAATTTTGGAGGGT 360
QY 361 TTTCACAGGAGAGCTTATCTTTATATCTGCTTACACAGCAGCAAACTGGCAG 420
DB 361 TTTCACAGGAGAGCTTATCTTTATATCTGCTTACACAGCAGCAAACTGGCAG 420
QY 421 GTGTCACTGACAGCTTCTTCTTCCACTTGGGNTTCTTCCACAGGKCTATCG 480
DB 421 GTGTCACTGACAGCTTCTTCTTCCACTTGGGNTTCTTCCACAGGKCTATCG 480
QY 481 GTGTGCTAATATAGATATTTCTATCTCAGTGCACAGGGGATTTGACCTTTGGTTC 540
DB 481 GTGTGCTAATATAGATATTTCTATCTCAGTGCACAGGGGATTTGACCTTTGGTTC 540
QY 541 CCTGATGTTGGTCTCTTACGGTGGAAAACTAAACATTTGGATTCAGCCCAATG 600
DB 541 CCTGATGTTGGTCTCTTACGGTGGAAAACTAAACATTTGGATTCAGCCCAATG 600
QY 601 TGACCTTTAAACCTATGAAGATATGACAGATCTGTCTCAACAGGAATGATGATG 660
DB 601 TGACCTTTAAACCTATGAAGATATGACAGATCTGTCTCAACAGGAATGATGATG 660
QY 661 TCAAGCAATTCATTTGATTAACCTCTACCTTCAATTTGATTTGACGTACTA 709
DB 661 TCAAGCAATTCATTTGATTAACCTCTACCTTCAATTTGATTTGACGTACTA 709

RESULT 3
AR104346 709 bp DNA linear PAT 14-FEB-2001
LOCUS AR104346
DEFINITION Sequence 2 from patent US 6093561.
ACCESSION AR104346
VERSION AR104346.1 GI:12817054
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 709)
AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
TITLE Human lysophospholipase
JOURNAL Patent: US 6093561-A 2 25-JUL-2000;
FEATURES Location/Qualifiers

source 1..709
/organism="unknown"
BASE COUNT 166 a 169 c 175 g 197 t 2 others
ORIGIN

Query Match 99.8%; Score 707.6; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 4e-176;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGCTGCACGCCCTTGGGCGCGGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 60
DB 1 GCCGCTGCACGCCCTTGGGCGCGGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 60
QY 61 AGCTAGAGCGGCTGATGTGCGGCAATACATGTCAACCCCGCTGCCCGCCATCGTCCCG 120
DB 61 AGCTAGAGCGGCTGATGTGCGGCAATACATGTCAACCCCGCTGCCCGCCATCGTCCCG 120
QY 121 CCGCCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGATGATGAGATGAGTGGGCTG 180
DB 121 CCGCCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGATGATGAGATGAGTGGGCTG 180
QY 181 TTAGGCTGTACATTAATATGAACGTGCTATGCTTCAATGGTTGATATTTATTTGGGC 240
DB 181 TTAGGCTGTACATTAATATGAACGTGCTATGCTTCAATGGTTGATATTTATTTGGGC 240
QY 241 TTTCACGATTTACAGAGAGATGATCTGGATTTAAACAGGAGAGAAATATATAAG 300
DB 241 TTTCACGATTTACAGAGAGATGATCTGGATTTAAACAGGAGAGAAATATATAAG 300
QY 301 CTTTGATTTGATCAAGAAATGAAGATGAGATTCCTTCAACAGATTAATTTTGGAGGGT 360
DB 301 CTTTGATTTGATCAAGAAATGAAGATGAGATTCCTTCAACAGATTAATTTTGGAGGGT 360
QY 361 TTTCACGAGAGAGAGCTTATCTTATATCTGCTTACACACAGCAGAAACTGGCAG 420
DB 361 TTTCACGAGAGAGAGCTTATCTTATATCTGCTTACACACAGCAGAAACTGGCAG 420
QY 421 GTGTACAGCAGCTAGTTCTTGGCTTCCACTTGGGANTTCTTCCACAGGAGCTATG 480
DB 421 GTGTACAGCAGCTAGTTCTTGGCTTCCACTTGGGANTTCTTCCACAGGAGCTATG 480
QY 481 GTGTGCTAATAGAGATATTTCTATCTCCAGTGCACAGGGGATTTGACCCCTTGGTTC 540
DB 481 GTGTGCTAATAGAGATATTTCTATCTCCAGTGCACAGGGGATTTGACCCCTTGGTTC 540
QY 541 CCTGATGTTGGTCTCTTACGGTGAAGAAACATTAACATTTGTAATCCACCAATG 600
DB 541 CCTGATGTTGGTCTCTTACGGTGAAGAAACATTAACATTTGTAATCCACCAATG 600
QY 601 TGACCTTTAAACCTATGAGATGATGACAGCTGCTGTCACAGAGAAATGATGATG 660
DB 601 TGACCTTTAAACCTATGAGATGATGACAGCTGCTGTCACAGAGAAATGATGATG 660
QY 661 TCAAGCAATTCATTGATTAACCTCCTACCTCAATTTGATGACGTCACTA 709
DB 661 TCAAGCAATTCATTGATTAACCTCCTACCTCAATTTGATGACGTCACTA 709

RESULT 4
ARI78569
LOCUS ARI78569 709 bp DNA linear PAT 20-Apr-2002
DEFINITION Sequence 2 from patent US 6319701.
ACCESSION ARI78569
VERSION ARI78569.1 GI:20219707
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 709)
AUTHORS Hillman,J.L., Shah,P. and Murry,L.E.
TITLE Human lymphospholipase
JOURNAL Patent: US 6319701-A 2 20-NOV-2001;
FEATURES Location/Qualifiers

source 1..709
/organism="unknown"
BASE COUNT 166 a 169 c 175 g 197 t 2 others
ORIGIN

Query Match 99.8%; Score 707.6; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 4e-176;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGCTGCACGCCCTTGGGCGCGGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 60
DB 1 GCCGCTGCACGCCCTTGGGCGCGGCGCGCGCGCTTCTTCCGCTTGGCGCTGTG 60
QY 61 AGCTAGAGCGGCTGATGTGCGGCAATACATGTCAACCCCGCTGCCCGCCATCGTCCCG 120
DB 61 AGCTAGAGCGGCTGATGTGCGGCAATACATGTCAACCCCGCTGCCCGCCATCGTCCCG 120
QY 121 CCGCCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGATGATGAGATGAGTGGGCTG 180
DB 121 CCGCCCGGAAGGCCACCGCTGCGGTGATTTCTGCAATGATGATGAGATGAGTGGGCTG 180
QY 181 TTAGGCTGTACATTAATATGAACGTGCTATGCTTCAATGGTTGATATTTATTTGGGC 240
DB 181 TTAGGCTGTACATTAATATGAACGTGCTATGCTTCAATGGTTGATATTTATTTGGGC 240
QY 241 TTTCACGATTTACAGAGAGATGATCTGGATTTAAACAGGAGAGAAATATATAAG 300
DB 241 TTTCACGATTTACAGAGAGATGATCTGGATTTAAACAGGAGAGAAATATATAAG 300
QY 301 CTTTGATTTGATCAAGAAATGAAGATGAGATTCCTTCAACAGATTAATTTTGGAGGGT 360
DB 301 CTTTGATTTGATCAAGAAATGAAGATGAGATTCCTTCAACAGATTAATTTTGGAGGGT 360
QY 361 TTTCACGAGAGAGAGCTTATCTTATATCTGCTTACACACAGCAGAAACTGGCAG 420
DB 361 TTTCACGAGAGAGAGCTTATCTTATATCTGCTTACACACAGCAGAAACTGGCAG 420
QY 421 GTGTACAGCAGCTAGTTCTTGGCTTCCACTTGGGANTTCTTCCACAGGAGCTATG 480
DB 421 GTGTACAGCAGCTAGTTCTTGGCTTCCACTTGGGANTTCTTCCACAGGAGCTATG 480
QY 481 GTGTGCTAATAGAGATATTTCTATCTCCAGTGCACAGGGGATTTGACCCCTTGGTTC 540
DB 481 GTGTGCTAATAGAGATATTTCTATCTCCAGTGCACAGGGGATTTGACCCCTTGGTTC 540
QY 541 CCTGATGTTGGTCTCTTACGGTGAAGAAACATTAACATTTGTAATCCACCAATG 600
DB 541 CCTGATGTTGGTCTCTTACGGTGAAGAAACATTAACATTTGTAATCCACCAATG 600
QY 601 TGACCTTTAAACCTATGAGATGATGACAGCTGCTGTCACAGAGAAATGATGATG 660
DB 601 TGACCTTTAAACCTATGAGATGATGACAGCTGCTGTCACAGAGAAATGATGATG 660
QY 661 TCAAGCAATTCATTGATTAACCTCCTACCTCAATTTGATGACGTCACTA 709
DB 661 TCAAGCAATTCATTGATTAACCTCCTACCTCAATTTGATGACGTCACTA 709

RESULT 5
AX018183
LOCUS AX018183 2408 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 156 from Patent WO946374.
ACCESSION AX018183
VERSION AX018183.1 GI:10042561
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilsarsky,C.
TITLE Human nucleic acid sequences from prostate tumour tissue

OY	176	-----GCGTTAGGCGCTTTCATTTAAATTAATGAACGTGGCTATGCCCTCATGGTTGGATATTA	234
Db	261	CCCCTGTTAGGCGCTTTCATTTAAATTAATGAACGTGGCTATGCCCTCATGGTTGGATATTA	320
OY	235	TTGGGCTTTCACCAATTCACAGAGAGATGAATCTGGGATTAAACAGGACAGAAAAATA	294
Db	321	TTGGGCTTTCACCAAGATTTCACAGAGAGATGAATCTGGGATTAAACAGGACAGAAAAATA	380
OY	235	TAAAGCTTATATGATCAAGAGAGAGATNGCATTCCTCTAACAAGATATATTTGG	354
Db	361	TAAAGCTTATATGATCAAGAGAGAGATNGCATTCCTCTAACAAGATATATTTGG	440
OY	355	GAGGCTTTTCACAGGAGAGAGCTTTATCTTATATATACGCCCTTACCAACAGCAAGAAC	414
Db	441	GAGGCTTTTCACAGGAGAGAGCTTTATCTTATATATACGCCCTTACCAACAGCAAGAAC	500
OY	415	TGGCAGGCTGTCACATCACTAGTTCTTGTCCTCCACTTCGGGNTTCCTTCCACAGGKRC	474
Db	501	TGGCAGGCTGTCACATCACTAGTTCTTGTCCTCCACTTCGGGNTTCCTTCCACAGGKRC	560
OY	475	CTATCGAGTGATGCTAATAGAGATATTTCTATCTTCCAGTGCACACGGGATGTGACCCCT	534
Db	561	CTATCGAGTGATGCTAATAGAGATATTTCTATCTTCCAGTGCACACGGGATGTGACCCCT	620
OY	535	TGCTCCCGCCCTGATGTTTGGTCTCTTACGGGTGGAAAACTAAAAACATTGGTGATCCAG	594
Db	621	TGCTCCCGCCCTGATGTTTGGTCTCTTACGGGTGGAAAACTAAAAACATTGGTGATCCAG	680
OY	595	CCAATGTACCTTTAAAACTATGAAGGTATGATGCACAGTTCGCTCAACAGGAAATGA	654
Db	681	CCAATGTACCTTTAAAACTATGAAGGTATGATGCACAGTTCGCTCAACAGGAAATGA	740
OY	655	TGGATGTCAACCAATTCATTGATATAACTCTTAACCTCCAAATGATTTGAGCTCACTA	709
Db	741	TGGATGTCAACCAATTCATTGATATAACTCTTAACCTCCAAATGATTTGAGCTCACTA	795

[illegible]

OY	176	-----	175
Db	182	GATGGGCAAGACCCTTGACAGTATCAGAGTTCACATATCAATATATATCTGCCGATG	241
OY	176	-GCCTGTAGGCGCTTACATTAATATATGAACGTGGCTATGCTTCATGGTTGATATTA	234
Db	242	CCCCTGTAGGCGCTTACATTAATATATGAACGTGGCTATGCTTCATGGTTGATATTA	301
OY	235	TTGGGCTTTACACGATTCACAGAGAGATGAATCTGGGATTAACAGCGCAGCAAAAATA	294
Db	302	TTGGGCTTTACACGATTCACAGAGAGATGAATCTGGGATTAACAGCGCAGCAAAAATA	361
OY	295	TAAAGCTTTGATTTGATCAAGAAAGTGAAGAAAGGATTCCTCTAAGCAATATATTTGG	354
Db	362	TAAAGCTTTGATTTGATCAAGAAAGTGAAGAAAGGATTCCTCTAAGCAATATATTTGG	421
OY	355	GAGGGTTTTCTCAGAGGAGAGCTTATGCTTTATATATACGCCCTTACACAGCAGCAAAAC	414
Db	422	GAGGGTTTTCTCAGAGGAGAGAGCTTATGCTTTATATATACGCCCTTACACAGCAGCAAAAC	481
OY	415	TGGCAGGTGTCACAGCTCAGTTCTTGGCTTCACACTTGGGGTTCCTTCCACAGGKC	474
Db	482	TGGCAGGTGTCACAGCTCAGTTCTTGGCTTCACACTTGGGGTTCCTTCCACAGGKC	541
OY	475	CTATGGGTGGTCTATATGAGATATTTCATCTCCAGGCGCAGGGGATTTGTGACCCCT	534
Db	542	CTATGGGTGGTCTATATGAGATATTTCATCTCCAGGCGCAGGGGATTTGTGACCCCT	601
OY	535	TGGTTCCCTCGATGTGTTGGTTCTCTTAGCGTGGAAAACTAAAAACATTTGGTGAATCCAG	594
Db	602	TGGTTCCCTCGATGTGTTGGTTCTCTTAGCGTGGAAAACTAAAAACATTTGGTGAATCCAG	661
OY	595	CCAAATGTGACCTTTAAAACTATGGAAGGTATGTCACACAGTTCGTGTCAACAGGAAATGA	654
Db	662	CCAAATGTGACCTTTAAAACTATGGAAGGTATGTCACACAGTTCGTGTCAACAGGAAATGA	721
OY	655	TGGATGTCAAGCAATTCATTTGATTAACATCCTACCTCCCAATTCATTTGAGCTCCTA	709
Db	722	TGGATGTCAAGCAATTCATTTGATTAACATCCTACCTCCCAATTCATTTGAGCTCCTA	776

LOCUS	AR104347	1486 bp	DNA	linear	PAT 14-FEB-2001
DEFINITION	Sequence 4 from patent US 6093561.				
ACCESSION	AR104347				
VERSION	AR104347.1	GI:12817055			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1486)				
AUTHORS	Hillman,J.L., Shah,P. and Murry,L.E.				
TITLE	Human lysophospholipase				
JOURNAL	Patent: US 6093561-A 4-25-JUL-2000;				
FEATURES	Location/Qualifiers				
Source	1..1486				
	/organism="unknown"				
BASE COUNT	418 a 304 c 300 g 459 t			5 others	
ORIGIN					
Query Match	88.6%;	Score 628.4;	DB 6;	Length 1486;	
Best Local Similarity	91.0%;	Pred. No. 3.8e-155;			
Matches 705; Conservative	1;	Mismatches 3;	Indels 66;	Gaps 1;	
1	GCCTCTCCACGCCCCCTTGGGCGCGCGGCGCCGCTCTTCCTTCGCGCTGGCGTGG	60			
2	GCCTCTCCACGCCCCCTTGGGCGCGCGGCGCCGCGCTCTTCCTTCGCGCTGGCGTGG	61			
61	AGCTGAGCGCGGTGATGTGCGGGCAATTAACATGTCAACCCCGCTGCGCGCATGTCGCCG	120			
62	AGCTGAGCGCGGTGATGTGCGGGCAATTAACATGTCAACCCCGCTGCGCGCATGTCGCCG	121			

QY 121 CGCCCGGAAGGCGACCGGCTGATTTCTCATGATGGATGGAGATACGCG----- 175
 DB 122 CGCCCGGAAGGCGACCGGCTGATTTCTCATGATGGATGGAGATACGCGCGACG 181
 QY 176 ----- 175
 DB 182 GATGGCAGAGAGCTTTCAGATATCAGAAAGTTACATATCAAAATATATCTGCCCGCATG 241
 QY 176 -GCCCTTTAGGCGCTTTACATTAATATGAAAGCTGCTATGCTTCATGCTTGGATTTA 234
 DB 242 CGCCTTTAGGCGCTTTACATTAATATGAAAGCTGCTATGCTTCATGCTTGGATTTA 301
 QY 235 TTGGGCTTTACACAGATTCACAGAGATGAATCTGGGATTTAAACAGGAGAGAGAAATA 294
 DB 302 TTGGGCTTTACACAGATTCACAGAGATGAATCTGGGATTTAAACAGGAGAGAGAAATA 361
 QY 295 TAAAGCTTTGATTTGATTCAGAAAGTGAAGATGGCATTCCTCTCTAAACAGATTTATTTTG 354
 DB 362 TAAAGCTTTGATTTGATTCAGAAAGTGAAGATGGCATTCCTCTCTAAACAGATTTATTTTG 421
 QY 355 GAGGCTTTCTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAAAC 414
 DB 422 GAGGCTTTCTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAAAC 481
 QY 415 TGGCAGGCTTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAGC 474
 DB 482 TGGCAGGCTTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAGC 541
 QY 475 CTATCGGTGTGCTTAATAGAGATTTCTTCTCAGTGCACAGGGGAGATTTGACCCCTT 534
 DB 542 CTATCGGTGTGCTTAATAGAGATTTCTTCTCAGTGCACAGGGGAGATTTGACCCCTT 601
 QY 535 TGGTTCCTCCATGATTTGCTTCTTCTTACGTGAGAAACATAAAACATTTGTCATTCAG 594
 DB 602 TGGTTCCTCCATGATTTGCTTCTTCTTACGTGAGAAACATAAAACATTTGTCATTCAG 661
 QY 595 CCAATGTGACCTTTAAACCTATGAGAGTATGACAGAGTGTGTCACAGAGAGATGA 654
 DB 662 CCAATGTGACCTTTAAACCTATGAGAGTATGACAGAGTGTGTCACAGAGAGATGA 721
 QY 655 TGGATGTCAAGCAATTCATTTGATTAACCTGCTACCTCCAAATTTGATGACGTCACTA 709
 DB 722 TGGATGTCAAGCAATTCATTTGATTAACCTGCTACCTCCAAATTTGATGACGTCACTA 776
 RESULT 9
 AR203099 1556 bp DNA linear PAT 20-JUN-2002
 LOCUS AR203099
 DEFINITION Sequence 18 from patent US 6365354.
 ACCESSION AR203099
 VERSION AR203099.1 GI:21499401
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1556)
 AUTHORS Bennett,C.Frank, and Wyatt,J.
 TITLE Antisense modulation of lysophospholipase I expression
 JOURNAL Patent: US 6365354-A 18 02-Apr-2002;
 FEATURES
 source 1..1556
 Location/Qualifiers
 BASE COUNT 423 a 324 c 350 g 459 t
 ORIGIN
 Query Match 88.6%; Score 628.4; DB 6; Length 1556;
 Best Local Similarity 91.0%; Pred. No. 3.8e-155;
 Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;
 QY 1 GCGGCTCGACGCGCTTTGGGCGCGGCGCGGCGCGCTTCCTCCGCTGCGCTGCG 60
 DB 121 GCGGCTCGACGCGCTTTGGGCGCGGCGCGGCGCGCTTCCTCCGCTGCGCTGCG 180

QY 61 AGCTGAGGCGGCTGATTTGTCGCAATATACATGTCACACCCCGCTGCCCGCGCG 120
 DB 181 AGCTGAGGCGGCTGATTTGTCGCAATATACATGTCACACCCCGCTGCCCGCGCG 240
 QY 121 CGCCCGGAAGGCGACCGGCTGATTTCTCATGATGGATGGAGATACGCG----- 175
 DB 241 CGCCCGGAAGGCGACCGGCTGATTTCTCATGATGGATGGAGATACGCGCGACG 300
 QY 176 ----- 175
 DB 301 GATGGCAGAGAGCTTTCAGATATCAGAAAGTTACATATCAAAATATATCTGCCCGCATG 360
 QY 176 -GCCCTTTAGGCGCTTTACATTAATATGAAAGCTGCTATGCTTCATGCTTGGATTTA 234
 DB 361 CGCCTTTAGGCGCTTTACATTAATATGAAAGCTGCTATGCTTCATGCTTGGATTTA 420
 QY 235 TTGGGCTTTACACAGATTCACAGAGATGAATCTGGGATTTAAACAGGAGAGAGAAATA 294
 DB 421 TTGGGCTTTACACAGATTCACAGAGATGAATCTGGGATTTAAACAGGAGAGAGAAATA 480
 QY 295 TAAAGCTTTGATTTGATTCAGAAAGTGAAGATGGCATTCCTCTCTAAACAGATTTATTTTG 354
 DB 481 TAAAGCTTTGATTTGATTCAGAAAGTGAAGATGGCATTCCTCTCTAAACAGATTTATTTTG 540
 QY 355 GAGGCTTTCTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAAAC 414
 DB 541 GAGGCTTTCTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAAAC 600
 QY 415 TGGCAGGCTTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAGC 474
 DB 601 TGGCAGGCTTCAGGAGAGAGCTTTATCTTTATATCTGCTTACACAGAGAGAGC 660
 QY 475 CTATCGGTGTGCTTAATAGAGATTTCTTCTCAGTGCACAGGGGAGATTTGACCCCTT 534
 DB 661 CTATCGGTGTGCTTAATAGAGATTTCTTCTCAGTGCACAGGGGAGATTTGACCCCTT 720
 QY 535 TGGTTCCTCCATGATTTGCTTCTTCTTACGTGAGAAACATAAAACATTTGTCATTCAG 594
 DB 721 TGGTTCCTCCATGATTTGCTTCTTCTTACGTGAGAAACATAAAACATTTGTCATTCAG 780
 QY 595 CCAATGTGACCTTTAAACCTATGAGAGTATGACAGAGTGTGTCACAGAGAGATGA 654
 DB 781 CCAATGTGACCTTTAAACCTATGAGAGTATGACAGAGTGTGTCACAGAGAGATGA 840
 QY 655 TGGATGTCAAGCAATTCATTTGATTAACCTGCTACCTCCAAATTTGATGACGTCACTA 709
 DB 841 TGGATGTCAAGCAATTCATTTGATTAACCTGCTACCTCCAAATTTGATGACGTCACTA 895
 RESULT 10
 AF052112 1556 bp mRNA linear PRI 05-AUG-1998
 LOCUS AF052112
 DEFINITION Homo sapiens clone 23753 mRNA sequence.
 ACCESSION AF052112
 VERSION AF052112.1 GI:3360419
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 REFERENCE 1 (bases 1 to 1556)
 AUTHORS Anderson,B., Wentland,M.A., Ricafente,J.Y., Liu,W., and Gibbs,R.A.
 TITLE A 'double adaptor' method for improved shotgun library construction
 JOURNAL Anal. Biochem. 236 (1), 107-113 (1996)
 MEDLINE 96207227
 PUBMED 8619474
 YU,W., Anderson,B., Worley,R.C., Muzny,D.M., Ding,Y., Liu,W.,
 Ricafente,J.Y., Wentland,M.A., Lennon,G., and Gibbs,R.A.,
 Large-scale concatenation cDNA sequencing
 Genome Res. 7 (4), 353-358 (1997)
 JOURNAL 97264341
 MEDLINE 9110174
 PUBMED


```

Db      661 GTTCGTGTCACAGAAATGATGATGTCAGCAATTCATTAATCTCCTACCCAA 720
QY      694 TTGATTGAGTCACCTA 709
        |||||||
Db      721 TTGATTGAGTCACCTA 736

RESULT 12
AX256070
LOCUS    AX256070          2417 bp    DNA        linear    PAT 10-OCT-2001
DEFINITION Sequence 221 from Patent WO0170976.
ACCESSION AX256070
VERSION   AX256070.1 GI:16075110
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2417)
AUTHORS   Xu,J., Pyle,R.A. and Stolk,J.A.
TITLE     Compositions and methods for the therapy and diagnosis of ovarian
           and endometrial cancer
JOURNAL   Patent: WO 0170976-A 221 27-SEP-2001;
           CORIXA CORPORATION (US)
FEATURES
           source          1..2417
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
BASE COUNT 752 a 414 c 422 g 829 t
ORIGIN

Query Match      83.1%; Score 589.4; DB 6; Length 2417;
Best Local Similarity 90.5%; Pred. No. 8.2e-145;
Matches 666; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY      40 CTTCCTTCGGCTTGGCTGTGAGCTGTGAGCGGTGTATGTGGCGCAATAATGTCACACC 99
        |||||||
Db      1 CTTCCTTCGGCTTGGCTGTGAGCTGTGAGCGGTGTATGTGGCGCAATAATGTCACACC 60

QY      100 CGCTGCCGCCCATCGTGGCGCGCGCGCGCGGAGAGCCACCGCTGGGATTTCTTCGCAATG 159
        |||||||
Db      61 CGCTGCCGCCCATCGTGGCGCGCGCGCGCGGAGAGCCACCGCTGGGATTTCTTCGCAATG 120

QY      160 GATTGGAGACTACTG----- 175
        |||||||
Db      121 GATTGGAGACTACTGCGAGGATGGGAGAGCCCTTTCAGAGTATTCAGAAATTCACATA 180
        |||||||
QY      176 -----GCCTGTAGGCTGTTCATTAATTAATGAACGTGGCTA 213
        |||||||
Db      181 TCAAAATATATCTGCCCGATGCGCTGTGAGCTGTTCATTAATTAATGAACGTGGCTA 240

QY      214 TGCCCTTCATGTTTGTATTTATTTGGCTTTCACAGATTTACAGAGAGTGAATCTGGGA 273
        |||||||
Db      241 TGCCCTTCATGTTTGTATTTATTTGGCTTTCACAGATTTACAGAGAGTGAATCTGGGA 300

QY      274 TTAACAGGACAGAAAAATATAAAGCTTTGATTGATTCAGAAAGTGAAGATGGCATTC 333
        |||||||
Db      301 TTAACAGGACAGAAAAATATAAAGCTTTGATTGATTCAGAAAGTGAAGATGGCATTC 360

QY      334 CTTCACAGAAATATTTTGGGAGGTTTTCACAGAGAGAGCTTTATCTTTATCTACTGC 393
        |||||||
Db      361 CTTCACAGAAATATTTTGGGAGGTTTTCACAGAGAGAGCTTTATCTTTATCTACTGC 420

QY      394 GCCTTACACAGAGAGAAACTGAGAGGTCTACAGCTAGTCTTCTGCTTCACATTC 453
        |||||||
Db      421 CCCTTACACAGAGAGAAACTGAGAGGTCTACAGCTAGTCTTCTGCTTCACATTC 480

QY      454 GGGATTCCTTTCACAGAGGKCTATCGGTGAGTAAATAGAGATTTCTATTCCTCCAGT 513
        |||||||
Db      481 GGGATTCCTTTCACAGAGGKCTATCGGTGAGTAAATAGAGATTTCTATTCCTCCAGT 540

QY      514 GCCACGGGATTTGACCTTTGGTCCCTGATGTTGGTCTCTTACGGTGAAGAAAC 573
        |||||||

```

```

Db      541 GCCACGGGATTTGACCTTTGGTCCCTGATGTTGGTCTCTTACGGTGAAGAAAC 600
QY      574 TAAACATTTGGTGAATCCACGCAATGTGACCTTTAAACCTATGAAGATGATGCACA 633
        |||||||
Db      601 TAAACATTTGGTGAATCCACGCAATGTGACCTTTAAACCTATGAAGATGATGCACA 660

QY      634 GTTCGTGTCACAGAAATGATGATGTCAGCAATTCATTAATCTCCTACCTCAAA 693
        |||||||
Db      661 GTTCGTGTCACAGAAATGATGATGTCAGCAATTCATTAATCTCCTACCTCAAA 720

QY      694 TTGATTGAGTCACCTA 709
        |||||||
Db      721 TTGATTGAGTCACCTA 736

RESULT 13
AF081281
LOCUS    AF081281          2417 bp    mRNA        linear    PRI 13-AUG-1998
DEFINITION Homo sapiens lysophospholipase (LpL1) mRNA, complete cds.
ACCESSION AF081281
VERSION   AF081281.1 GI:3415122
KEYWORDS
SOURCE    Homo sapiens.
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2417)
AUTHORS   Hu,G.
TITLE     Direct Submission
JOURNAL   Submitted (02-AUG-1998) Shanghai Institute of Cell Biology, 320
           Yue-Yang Road, Shanghai 200031, China
FEATURES
           source          1..2417
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
           gene           1..2417
                        /gene="LpL1"
                        /gene="LpL1"
                        /gene="LpL1"
                        /codon_start=1
                        /product="Lysophospholipase"
                        /protein_id="AAC31610.1"
                        /db_xref="GI:3415123"
                        /translation="MCGNNMSTPELPAIVPAARKATPAVIFLGLDPTGMAEAFAGI
                        RSSKIRYICHPHARVPTLNMVAMPMSWDIIGLSPDSOEDSGIKQAEENKALIDG
                        EVKNGIPSNMIIIGRPSOGGASLYALTLTQKLGVTLSQMLPRLRSFPGCGIGA
                        NRDISLQGGDDPLVPLMFGSLYVEKLTIVNPAVTFKTYEGMHSSCOENMADV
                        KQFDKLPDID"
BASE COUNT 752 a 414 c 422 g 829 t
ORIGIN

Query Match      83.1%; Score 589.4; DB 9; Length 2417;
Best Local Similarity 90.5%; Pred. No. 8.2e-145;
Matches 666; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY      40 CTTCCTTCGGCTTGGCTGTGAGCTGTGAGCGGTGTATGTGCGCAATTAACATGTCACACC 99
        |||||||
Db      1 CTTCCTTCGGCTTGGCTGTGAGCTGTGAGCGGTGTATGTGCGCAATTAACATGTCACACC 60

QY      100 CGTGGCCGCCCATGTCGCCCGCGCGCGGAGAGCCACCGCTGGGATTTCTTCGCAATG 159
        |||||||
Db      61 CGTGGCCGCCCATGTCGCCCGCGCGCGGAGAGCCACCGCTGGGATTTCTTCGCAATG 120

QY      160 GATTGGAGACTACTG----- 175
        |||||||
Db      121 GATTGGAGACTACTGCGAGGATGGGAGAGCTTTGCAGGTATTCAGAAATTCACATA 180

QY      176 -----GCCTGTAGGCTGTTCATTAATTAATGAAGTGGCTA 213
        |||||||
Db      181 TCAAAATATCTGCCCGATGCGCTGTGAGCTGTTCATTAATTAATGAAGTGGCTA 240

QY      214 TGCCCTTCATGTTTGTATTTATTTGGCTTTCACAGATTTACAGAGAGTGAATCTGGGA 273
        |||||||

```

Db 241 TGCTTACGTTGATATATATGGGCTTTCACCAATTCACAGAGGATGAATCTGGGA 300
 QY 274 TTAACAGGACGAGAAATATATAAGCTTGGATGATCAAGAGTGAAGATGGCAATTC 333
 Db 301 TTAACAGGACGAGAAATATATAAGCTTGGATGATCAAGAGTGAAGATGGCAATTC 360
 QY 334 CTCTAAGAGAAATATATGGAGGCTTTCACAGGAGAGCTTATCTTATATATCTG 393
 Db 361 CTCTAAGAGAAATATATGGAGGCTTTCACAGGAGAGCTTATCTTATATATCTG 420
 QY 394 CCCTTACACACAGCAAGAACTGGCAGGTGTCACTGCACTGATCTTCTCTCCACTTC 453
 Db 421 CCCTTACACACAGCAAGAACTGGCAGGTGTCACTGCACTGATCTTCTCTCCACTTC 480
 QY 454 GGGATCTCTTCCACAGGAGGCTTATCGGTGTCTAATAGATATTTCTTCTCCAGT 513
 Db 481 GGGCTCTCTTCCACAGGAGGCTTATCGGTGTCTAATAGATATTTCTTCTCCAGT 540
 QY 514 GCCACGGGATGTGACCTTGGTTCCTGATGTTGGTCTTCTTACGGTGGAAAAAC 573
 Db 541 GCCACGGGATGTGACCTTGGTTCCTGATGTTGGTCTTCTTACGGTGGAAAAAC 600
 QY 574 TAAACATTTGGTGAATCCAGCAATGTGACCTTTAAAACTATGAAGATGATGACACA 633
 Db 601 TAAACATTTGGTGAATCCAGCAATGTGACCTTTAAAACTATGAAGATGATGACACA 660
 QY 634 GTTCTGTCAACAGAAATGATGATGTCAAGCAATTTATGATTAATCTTACTCTCA 693
 Db 661 GTTCTGTCAACAGAAATGATGATGTCAAGCAATTTATGATTAATCTTACTCTCA 720
 QY 694 TTGATTGACGTCACTA 709
 Db 721 TTGATTGACGTCACTA 736

RESULT 14
 AL365267 49616 bp DNA linear PRI 16-OCT-2000
 LOCUS Human DNA sequence from clone RP11-789A7 on chromosome 6, complete
 DEFINITION
 accession AL365267
 version AL365267.11 GI:10862783
 keywords HTG.
 source human.
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Williams, S.
 TITLE Submitted (16-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
 JOURNAL CB10 15A, UK. E-mail enquiries: humquerry@sanger.ac.uk
 COMMENT
 Requests: clonerequest@sanger.ac.uk
 On Oct 17, 2000 this sequence version replaced gi:10798380.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated human repeat sequence elements (e.g. Alu) where the
 sequence is ambiguous, there is an annotation using the 'unsure'
 feature key.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep this sequence
 was generated from part of bacterial clone contigs of human
 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping

Group. Further information can be found at
<http://www.sanger.ac.uk/BGP/Chr6>
 RP11-789A7 is from the library RPCT-11.3 constructed at the Roswell
 Park Cancer Institute by the group of Pieter de Jong. For further
 details see <http://bacpac.med.buffalo.edu/>
 VECTOR: pBACE3.6
 IMPORTANT: This sequence is not the entire insert of clone
 RP11-789A7. It may be shorter because we sequence overlapping
 sections only once, except for a 100 base overlap.
 The true right end of clone RP11-789A7 is at 49616 in this
 sequence. The true right end of clone RP1-20M4 is at 100 in this
 sequence.

FEATURES

source
 Location/Qualifiers
 1..49616
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="RP11-789A7"
 /clone_11b="RPCT-11.3"
 3..1917
 /note="LIM4 repeat: matches 4426..6289 of consensus"
 1923..2162
 /note="AluSq repeat: matches 1..256 of consensus"
 2192..2757
 /note="LIM4 repeat: matches 4331..4935 of consensus"
 3144..3283
 /note="LIM4 repeat: matches 3806..3957 of consensus"
 3638..3714
 /note="L2 repeat: matches 2663..2749 of consensus"
 3830..3997
 /note="84 copies 2 mer tt 58% conserved"
 complement(5884..6360)
 /note="match: GSS: Em:AQ512551"
 5997..6040
 /note="11 copies 4 mer tatt 100% conserved"
 6374..7030
 /note="match: GSS: Em:AQ350934"
 7218..7316
 /note="L2 repeat: matches 2617..2708 of consensus"
 7329..7423
 /note="MIR repeat: matches 50..157 of consensus"
 9372..9415
 /note="22 copies 2 mer tt 75% conserved"
 9417..9463
 /note="LIPAT repeat: matches 6094..6140 of consensus"
 9548..9697
 /note="MIR repeat: matches 55..210 of consensus"
 10693..10791
 /note="MER5A repeat: matches 43..166 of consensus"
 10725..10817
 /note="MER5A repeat: matches 10..102 of consensus"
 10855..10894
 /note="10 copies 4 mer cttt 90% conserved"
 10964..11009
 /note="MIR repeat: matches 145..191 of consensus"
 11025..11151
 /note="MER5A repeat: matches 9..124 of consensus"
 11152..11438
 /note="AluSx repeat: matches 1..306 of consensus"
 11439..11501
 /note="MER5A repeat: matches 124..189 of consensus"
 12041..12128
 /note="44 copies 2 mer gt 76% conserved"
 12073..12128
 /note="14 copies 4 mer gtgt 89% conserved"
 13157..13194
 /note="19 copies 2 mer tg 81% conserved"
 complement(14043..14525)
 /note="match: GSS: Em:AQ670292"
 14875..15196
 /note="MSTA repeat: matches 1..353 of consensus"
 15708..15749
 /note="21 copies 2 mer tg 92% conserved"

repeat_region	15710. .15749	/note="10 copies 4 mer tctg 95% conserved"
repeat_region	15809. .15962	/note="L1M01 repeat: matches 6067. .6223 of consensus"
repeat_region	15965. .16571	/note="L1M02 repeat: matches 5598. .6181 of consensus"
repeat_region	1908. .20251	/note="MHB repeat: matches 1. .364 of consensus"
misc_feature	complement(122475..22980)	/note="match: GSS: Em:547838"
misc_feature	complement(122534..23017)	/note="match: GSS: Em:AQ706688"
misc_feature	complement(122578..23017)	/note="match: GSS: Em:AQ822383"
repeat_region	22633. .22912	/note="AluNb repeat: matches 1. .290 of consensus"
repeat_region	22944. .23348	/note="L1M12 repeat: matches 1413. .1008 of consensus"
misc_feature	23015. .23496	/note="match: GSS: Em:AQ320567"
misc_feature	23020. .23582	/note="match: GSS: Em:AQ420187"
misc_feature	23022. .23744	/note="match: GSS: Em:AQ386439"
repeat_region	23357. .23413	/note="L1M12 repeat: matches 6107. .6164 of consensus"
repeat_region	23500. .24017	/note="L1M01 repeat: matches 5661. .6216 of consensus"
repeat_region	24016. .24847	/note="L1M repeat: matches 2418. .3266 of consensus"
repeat_region	24857. .25412	/note="L1M6 repeat: matches 1978. .2195 of consensus"
repeat_region	25413. .25716	/note="AluXc repeat: matches 1. .302 of consensus"
repeat_region	25717. .25986	/note="L1M6c repeat: matches 1702. .1978 of consensus"
repeat_region	25985. .26650	/note="L1M0 repeat: matches 0. .970 of consensus"
repeat_region	27281. .27322	/note="21 copies 2 mer gt 76% conserved"
repeat_region	29921. .30090	/note="L2 repeat: matches 2389. .2551 of consensus"
repeat_region	30162. .30324	/note="MER3 repeat: matches 3. .169 of consensus"
repeat_region	30370. .30462	/note="MER3 repeat: matches 126. .209 of consensus"
repeat_region	30419. .30469	/note="MER3 repeat: matches 41. .90 of consensus"
repeat_region	30639. .30803	/note="MIR repeat: matches 29. .201 of consensus"
repeat_region	30889. .31291	/note="WSTB repeat: matches 1. .422 of consensus"
repeat_region	32015. .32129	/note="MIR repeat: matches 35. .153 of consensus"
repeat_region	33754. .34173	/note="L2 repeat: matches 2238. .2705 of consensus"
repeat_region	34289. .34424	/note="L2 repeat: matches 1533. .1696 of consensus"
repeat_region	34893. .34999	/note="U6 repeat: matches 1. .107 of consensus"
repeat_region	35004. .36835	/note="MER3A repeat: matches 6. .106 of consensus"
repeat_region	40627. .40838	/note="L1M4 repeat: matches 2674. .2879 of consensus"
repeat_region	40839. .41142	/note="Alu0 repeat: matches 1. .301 of consensus"
repeat_region	41143. .41477	/note="L1M4 repeat: matches 2879. .3234 of consensus"
repeat_region	41522. .41805	

	repeat_region	/note="LIM4 repeat: matches 3390. .3673 of consensus" 41958. 42264 /note="AluSc repeat: matches 1. .306 of consensus" 42370. 42420 /note="Alu repeat: matches 242. .292 of consensus" 42721. 42845 /note="AluSg/x repeat: matches 19. .143 of consensus" 43491. 43616 /note="63 copies 2 mer aa 588 conserved" 43723. 43959 /note="LIMB3 repeat: matches 5943. .6181 of consensus" 44883. 44984 /note="51 copies 2 mer at 60% conserved" 45099. 45193 /note="MER21B repeat: matches 703. .790 of consensus" 45186. 45276 /note="MER21B repeat: matches 703. .794 of consensus" 45271. 46045
Query Match	Best Local Similarity	81.9%; Score 580.8; DB 9; Length 49616;
Matches 689;	Conservative	88.7%; Pred. No. 2,2e+142; Mismatches 19; Indels 68; Gaps 3
QY	1	GCCTGTCACGCGCTTGGCGCGCGCGCGCGCGCGCTTCCTTCCTTCGCGCTGCG 60
Db	17283	GCCTGTCACGCGCGCTTGGCGCGCGCGCGCGCGCGCTTCCTTCCTTCGCGCTGCG 17342
QY	61	AGCTGAGGCGGTATGTGTCGGCAATATGTCACCCGCGCGCGCGCGCGCGCGCGCG 120
Db	17343	AGCTGAGGCGGTATGTGTCGGCAATATGTCACCCGCGCGCGCGCGCGCGCGCGCG 17402
QY	121	CGCGCCGAGAGCCACGCGTGGGTATTTTCCTGCATGATTTGGAGATCTGCG---- 175
Db	17403	CGCGCCGAGAGCCACGCGTGGGTATTTTCCTGCATGATTTGGAGATCTGCGCGCG 17462
QY	176	----- 175
Db	17463	GATGGCGAGAGCGCTTGGCGCGGTATCATATGATTCACATATCAAAATATATCTGCCGATG 17522
QY	176	-GCGTGTATGAGCGCTGTT-ACATTAATATATGAACGTCGTCATGCTTCATGATTTGATAT 233
Db	17523	GCGTGTATGAGCGCTGTTATTAATATATGAACATATGATGCTTCATGATTTGATAT 17582
QY	234	ATTGGGCTTTCACACAGATTCACAGAGATGATCTGGATTTAAACAGCAGCAAAAT 293
Db	17583	ATTGGGCTTTCACACAGATTCACAGAGATGATCTGGATTTAAACAGCAGCAGCAAAAT 17642
QY	294	ATTAAGGCTTATTTGATATGAAGAAGAAAGATGCGATTCCTTTAAACGAATTTATTTG 353
Db	17643	ATTAAGGCTTATTTGATATGAAGAAGAAAGATGCGATTCCTTTAAACGAATTTATTTG 17702
QY	354	GGAGGCTTTTCACAGGAGAGCTTTATCTTATATATCTGCCCTTAACACAGCAGAGAA 413
Db	17703	GGAGGCTTTTCACAGGAGAGCTTTATCTTATATATCTGCCCTTAACACAGCAGAGAA 17762
QY	414	CGGCGAGGTGTACGCACTGCTTCCTTCCTTCACCTCGGGGANTTCCTTCCACAGGK 473
Db	17763	CGGCGAGGTGTACGCACTGCTTCCTTCCTTCACCTCGGGGANTTCCTTCCACAGGCT 17822
QY	474	CCTATCGGTGTGCTAAATAGAGATATTTCTATTCACAGTGCACAGGGGATTTGACCT 533
Db	17823	CCTATCGGTGTGCTAAATAGAGATATTTCTATTCACAGTGCACAGGGGATTTGACCT 17882
QY	534	TTGGTTCCCTGATGTTGGTTCTCTTCACGGTGGAGAAACT-AAAAACATTTGGTATCC 592
Db	17883	TTGGTTCCCTGATGTTGGTTCTCTTCACGGTGGAGAAACT-AAAAACATTTGGTATCC 17942
QY	593	ACCCATGAGCACTTAAACCTATGAAGGTATGATGACAGATTTGTCACAGAGAAAT 652
Db	17943	ACCCATGAGCACTTAAACCTATGAAGGTATGATGACAGATTTGTCACAGAGAAAT 18002
QY	653	GATGATGCAAGCAATTCATGATAACTCTTACCTCCAAATGATGATGACGACATA 709

Db 18003 GATGAATGTCAGCAATTCATTGATTAACCTCCTACCTCCATTGATTGACGTCACTA 18059

RESULT 15

AF291053 760 bp mRNA linear PRI 20-NOV-2000

LOCUS AF291053 Homo sapiens acyl-protein thioesterase-1 mRNA, complete cds.

DEFINITION AF291053

ACCESSION AF291053.1 GI:9965371

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 760) Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. Deredjiev, Y., Dauter, Z., Kuznetsov, S.R., Jones, T.L. and Dretwenda, Z.S.

TITLE Crystal structure of the human acyl protein thioesterase I from a single X-ray data set to 1.5 Å

JOURNAL MEDLINE 20535036

PubMed 11080636

REFERENCE 2 (bases 1 to 760) Kuznetsov, S.R. and Jones, T.L.Z.

AUTHORS Direct Submission

TITLE Submitted (28-JUL-2000) Metabolic Disease Branch, National Institute of Diabetes and Digestive and Kidney Diseases, 9000 Rockville Pike, Bldg. 10, Room 9C112, Bethesda, MD 20892, USA

FEATURES

source location/Qualifiers

1..760

/organism="Homo sapiens"

/db_xref="taxon:9606"

19..711

/note="hydrolase; APT-1"

/codon_start=1

/evidence="not_experimental"

/product="acyl-protein thioesterase-1"

/protein_id="AAG10063.1"

/db_xref="GI:9965372"

/translation="MCGNNMSTPLPAIVPAARKTAAYVFLHGLGDTGSHMAEFAGI RSHRTICPHAPVRYPLNKNVAMPWFIDIGLSPDSODESITKQAAENIKALIDQ EVKNGIPSNRIILIGFSQGALSLYTALITQOKLAGTALSCWLPRLASFPOGPIGA NRDISILQCHDDCDPLVPLMGSLVEKLTIVPANVTFKTEGMMHSSCOQEMMDV KQFIDKLPLPID"

misc_feature 34

/note="alternate site of translation initiation"

BASE COUNT 197 a 166 c 186 g 211 t

ORIGIN

Query Match 80.7%; Score 572.4; DB 9; Length 760;

Best Local Similarity 90.3%; Pred. No. 2,2e-140;

Matches 649; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

OY 57 TGTGAGCTGAGGCGGTGATGTGCGGCAATACATGTCACCCGCTGCCCATCGTG 116

DB 1 TGTGAGCTGAGGCGGTGATGTGCGGCAATACATGTCACCCGCTGCCCATCGTG 60

OY 117 CCGCGCGCGCGGGAAGGCCACCGCTGCGGTGATTTTCTGCAATGATGGAGATCTGG- 175

DB 61 CCGCGCGCGCGGGAAGGCCACCGCTGCGGTGATTTTCTGCAATGATGGAGATCTGGG 120

OY 176 ----- 175

DB 121 CACGATGGGCGAAGCCTTTGCGAGTATCAGAAGTTCACATATCAATATATCTGCCCG 180

OY 176 -----GCTGTAGGCTGTACATTAATATGAACGTGCTATGCTTCATGCTTTGAT 230

DB 181 CATGGCCTGTAGCGCTGTACATTAATATGAACGTGCTATGCTTCATGCTTTGAT 240

OY 231 ATTATTGGCTTTCACGATTCACAGAGATGATTTGGGATTTAAACAGGACGAGAA 290

DB 241 ATTATTGGCTTTCACGATTCACAGAGATGATTTGGGATTTAAACAGGACGAGAA 300

OY 291 AATAAAGCTTTGATTGATGATCAGAGATGAGATGGCATTCCTCTAACAGAAATTAT 350

DB 301 AATAAAGCTTTGATTGATGATCAGAGATGAGATGGCATTCCTCTAACAGAAATTAT 360

OY 351 TTGGAGAGCTTTTCTCAGGAGAGAGCTTTATCTTTATATACTAGCCCTTACACAGACAG 410

DB 361 TTGGAGAGCTTTTCTCAGGAGAGAGCTTTATCTTTATATACTAGCCCTTACACAGACAG 420

OY 411 AAATGCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 470

DB 421 AAATGCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480

OY 471 GGCCTATGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 530

DB 481 GGCCTATGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

OY 531 CTTTGGTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 590

DB 541 CTTTGGTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

OY 591 CCAGCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 650

DB 601 CCAGCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

OY 651 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 709

DB 661 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719

Search completed: January 19, 2003, 02:36:49

Job time : 3220 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 18, 2003, 23:46:20 ; Search time 301 Seconds
(without alignments)
Found 441 alignments)

Title: US-09-988-982-2

Perfect score: 709
Sequence: 1 GCCGCTGCACGCCCTTGGG.....CCATTGATTGACGTCACTA 709

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

```
Searched:      2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002.*

- 1: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1980.DAT.*
- 2: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1981.DAT.*
- 3: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1982.DAT.*
- 4: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1983.DAT.*
- 5: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1984.DAT.*
- 6: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1985.DAT.*
- 7: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1986.DAT.*
- 8: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1987.DAT.*
- 9: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1988.DAT.*
- 10: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1989.DAT.*
- 11: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1990.DAT.*
- 12: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1991.DAT.*
- 13: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1992.DAT.*
- 14: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1993.DAT.*
- 15: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1994.DAT.*
- 16: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1995.DAT.*
- 17: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1996.DAT.*
- 18: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1997.DAT.*
- 19: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1998.DAT.*
- 20: /SID52/gcgdata/geneseq/geneseqn.emb1/NA1999.DAT.*
- 21: /SID52/gcgdata/geneseq/geneseqn.emb1/NA2000.DAT.*
- 22: /SID52/gcgdata/geneseq/geneseqn.emb1/NA2001A.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseqn.emb1/NA2001B.DAT.*
- 24: /SID52/gcgdata/geneseq/geneseqn.emb1/NA2002.DAT.*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	707.6	99.8	709	20	AA556266	Human Iysoosphol
2	663	93.5	2396	22	AAH34424	Human colon cancer
3	628.4	88.6	1486	20	AA556267	Human Iysoosphol
4	628.4	88.6	1556	24	ABK37045	DNA encoding humaan
5	628.4	88.6	2493	21	AAAC98208	Human colon cancer
6	628.4	88.6	2600	23	ABV25207	Human prostate exp
7	606.4	85.5	1538	23	AA571464	DNA encoding novel
8	600.8	84.7	758	22	AAH26336	Human brain Iyso
9	589.4	83.1	2417	22	AA556597	Human cDNA for an

10	589.4	83.1	2417	24	ABL755314	Human lysophospholipid
11	589.4	83.1	2417	24	ABL755314	Human encoding human
12	561	79.1	1300	21	AAZ61501	CDNA encoding a hu
13	436	61.5	693	24	ABK37037	DNA encoding mouse
14	433.2	61.1	727	24	ABK37048	DNA encoding mouse
c 15	392.6	55.4	419	24	ABL37080	Human colon tumour
16	217.2	30.6	164	22	AAC60229	Human hydrolase-11
c 17	217.2	30.6	1647	24	ABL55935	Human lysophosphol
18	164	23.1	270	23	AAST71463	DNA encoding novel
19	130	18.3	183	20	AAZ35316	Human prostate can
20	126	17.8	782	22	AA556596	Human CDNA for an
21	119.8	16.9	461	22	AA556583	Human CDNA for an
22	97.8	13.8	363	21	AAH31022	Human colon cancer
23	93.4	13.2	1208	23	ABL21049	Drosophila melanog
24	90.6	12.8	608	24	ABK37047	DNA encoding mouse
c 25	88	12.4	3917	23	ABL21048	Drosophila melanog
c 26	64.2	9.1	62909	22	AAE28545	Genomic fragment #
c 27	57.6	8.1	545	21	AAAF15497	Aspergillus oryzae
c 28	55.8	7.9	589	24	ABLF6983	Pancreas cancer re
c 29	55.8	7.9	709	24	ABK34374	Human CDNA for nov
30	55.8	7.9	852	21	AAA87713	Secreted protein e
31	55.8	7.9	852	21	AAA87762	Human secreted prot
32	55.8	7.9	852	21	AAAC00014	Human secreted prot
33	55.8	7.9	852	21	AAZ42253	Human lysophosphol
34	55.8	7.9	852	22	AAAF63995	CDNA encoding secr
35	55.8	7.9	852	22	AAAF64044	CDNA encoding huma
36	55.8	7.9	975	20	AAX06946	Human lysophosphol
37	55.8	7.9	1861	23	ABV24194	Human prostate expr
38	55.8	7.9	1861	23	ABV25125	Human prostate expr
39	55.4	7.8	65	24	ABN53308	Mouse spliced tran
40	53.4	7.5	528	24	ABQ72633	Human MBDT encodin
c 41	51.8	7.3	604	24	ABO56978	Human colon cancer
c 42	40.4	5.7	273	20	AAAX4038	Human secreted pro
43	39.2	5.5	769	23	ABL11351	Drosophila melanog
44	39.2	5.5	2672	23	ABL07892	Drosophila melanog
45	39.2	5.5	2769	23	ABL11350	Drosophila melanog

ALIGNMENTS

RESULT 1
AAx56266
ID AAx56266 standard; cDNA; 709 BP.

DT 19-JUL-1999 (first entry)

Human lysophospholipase NHLP encoding cDNA.

KM Human: lysophospholipase; NHL: pcell proliferation; arteriosclerosis;
KM atherosclerosis; buritis; cirrhosis; hepatitis; myelofibrosis;
KM mixed connective tissue disease; paroxysmal nocturnal haemoglobinuria;
KM polycythaemia vera; psoriasis; primary thrombocytopenia; cancer;
KM inflammation; Addison's disease; AIDS; allergy; asthma; bronchitis;
KM immune response; ankylosing spondylitis; autoimmune haemolytic anaemia;
KM SS.

OS Homo sapiens.

Key	Location/Qualifiers
EH	75..709
FT	/tag= a
FT	/product= "NHLP"
FT	/note= "no stop codon given"
FT	

PN WO9849319-A1.

PD 05-NOV-1998.

PF 29-APR-1998; 98WO-US08782.

CC missing at time of publication, meaning no sequences are present for
CC Seq ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 2396 BP; 767 A; 402 C; 408 G; 816 T; 3 other;

Query Match 93.5%; Score 663; DB 22; Length 2396;
Best Local Similarity 99.0%; Pred. No. 2.5e-201;

Matches 663; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```

QY 40 CTTCTTCCTCCGCTTGGAGCTGAGCGGCTATGTCGGCATAACATGCAACC 99
   |||||
DB 1 CTTCTTCCTCCGCTTGGAGCTGAGCGGCTATGTCGGCATAACATGCAACC 60
   |||||
QY 100 CGGCGCCGCGGCTGCGCGCGCGGGAAGCGCGGCGGCTATGTCGGCATAAC 159
   |||||
DB 61 CGGCGCCGCGGCTGCGCGCGCGGGAAGCGCGCGGCTATGTCGGCATAAC 120
   |||||
QY 160 GATTGGAGATGAGCGGCTGTTAGCGCTGTACATTAATAATGAACGTCATGCTT 219
   |||||
DB 121 GATTGGAGATGAGCGGCTGTTAGCGCTGTACATTAATAATGAACGTCATGCTT 180
   |||||
QY 220 CATGCTTGTATTTATTTGGGCTTTCACAGATTCACAGAGATGAATCTGGATTAAC 279
   |||||
DB 181 CATGCTTGTATTTATTTGGGCTTTCACAGATTCACAGAGATGAATCTGGATTAAC 240
   |||||
QY 280 AGGAGAGAGAAATATATAAGCTTTGATTTGATTCAGAGAGATGAATGCGATTCCTCTA 339
   |||||
DB 241 AGGAGAGAGAAATATATAAGCTTTGATTTGATTCAGAGAGATGAATGCGATTCCTCTA 300
   |||||
QY 340 ACAGAAATTTATTTGGAGGCTTTCTCAGGAGAGGCTTTATCTTTATATCTGCCCTTA 399
   |||||
DB 301 ACAGAAATTTATTTGGAGGCTTTCTCAGGAGAGGCTTTATCTTTATATCTGCCCTTA 360
   |||||
QY 400 CCACACAGCAGAAACTGGCAGGCTGCTACCTGCTACTGCTTCTGCTTCCACTTGGGNTT 459
   |||||
DB 361 CCACACAGCAGAAACTGGCAGGCTGCTACCTGCTACTGCTTCTGCTTCCACTTGGGNTT 420
   |||||
QY 460 CTTTCCACAGGCGCTATGCTGCTGCTAATAGATATTTCTATCTCCAGTCCAGC 519
   |||||
DB 421 CTTTCCACAGGCGCTATGCTGCTGCTAATAGATATTTCTATCTCCAGTCCAGC 480
   |||||
QY 520 GGGATTTGACCCCTTTGGTTCCTCGATGTTGTTGCTCTTACGCGTGAATAAATA 579
   |||||
DB 481 GGGATTTGACCCCTTTGGTTCCTCGATGTTGTTGCTCTTACGCGTGAATAAATA 540
   |||||
QY 580 CATTGGTGAATCCAGCCAATGTGACTTTAAACCTTGAAGGTATGATGACAGTTCGT 639
   |||||
DB 541 CATTGGTGAATCCAGCCAATGTGACTTTAAACCTTGAAGGTATGATGACAGTTCGT 600
   |||||
QY 640 GTCAACAGGAATGATGATGTCAGCAATTCATTGATTAACCTCCATCCATTTGAT 699
   |||||
DB 601 GTCAACAGGAATGATGATGTCAGCAATTCATTGATTAACCTCCATCCATTTGAT 660
   |||||
QY 700 GAGCTCACTA 709
   |||||
DB 661 GAGCTCACTA 670
   |||||

```

RESULT 3
AA556267
ID AA556267 standard; cDNA; 1486 BP.

XX
AC AA556267;

XX 19-JUL-1999 (first entry)

DE Human lysophospholipase extended NHP encoding cDNA.

XX Human: lysophospholipase; NHP; cell proliferation; arteriosclerosis;
KM atherosclerosis; buritis; cirrhosis; hepatitis; myelofibrosis;
KM mixed connective tissue disease; paroxysmal nocturnal haemoglobinuria;
KW polycythemia vera; psoriasis; primary thrombocytopenia; cancer;
KW inflammation; Addison's disease; AIDS; allergy; asthma; bronchitis;

KW Immune response; ankylosing spondylitis; autoimmune haemolytic anaemia;
KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 76..768
FT CDS /tag= a
FT /product= "NHP"

XX W09849319-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98MO-US08782.

XX 12-FEB-1998; 98US-0022940.

XX 29-APR-1997; 97US-0844120.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Murry LE, Shah P;

XX WPI; 1999-326512/27.

XX P-PSDB; AAY09531.

XX New human lysophospholipase (NHP) polypeptides and polynucleotides

XX which identify and encode NHP

XX Claim 7; Fig 2; 66pp; English.

The present sequence encodes human lysophospholipase (NHP). The present invention also describes a method for treating or preventing a disorder of cell proliferation (e.g. arteriosclerosis, atherosclerosis, buritis, cirrhosis, hepatitis, mixed connective tissue disease, myelofibrosis, paroxysmal nocturnal haemoglobinuria, polycythemia vera, psoriasis, primary thrombocytopenia, and cancers), inflammation (e.g. Addison's disease, AIDS, allergies, asthma, atherosclerosis, bronchitis) and a disorder of the immune response (e.g. AIDS, allergies, ankylosing spondylitis, autoimmune haemolytic anaemia) by administering an antagonist to NHP. NHP proteins, antagonists, antibodies, agonists, complementary sequences or vectors may be administered in combination with other therapeutic agents. Antibodies which specifically bind to NHP may be used for the diagnosis of disorders characterized by expression of NHP or in assays to monitor patients being treated with NHP or agonists. The polynucleotides (PNS) encoding NHP or fragments may be used therapeutically. In one aspect, the complement of the CC polynucleotides may be used where it would be desirable to block the transcription of the mRNA. Complementary molecules may be used to CC modulate NHP activity or to achieve regulation of gene activity. CC Diagnostically, the PNS may be used to detect and quantitate gene CC expression in biopsied tissues in which expression of NHP may be CC correlated with disease.

XX Sequence 1486 BP; 418 A; 304 C; 300 G; 459 T; 5 other;

Query Match 88.6%; Score 628.4; DB 20; Length 1486;

Best Local Similarity 91.0%; Pred. No. 2.3e-190;

Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

```

QY 1 GCGGCTCGACAGCCCTTTGGGCGCGCGCGCGGCTCTTCCCTTGGCGGTGG 60
   |||||
DB 2 GCGGCTCGACAGCCCTTTGGGCGCGCGCGCGGCTCTTCCCTTGGCGGTGG 61
   |||||
QY 61 AGCTGAGCGGTGTATGTGGCGCAATACATGTCAACCCCGCTGCCGCAATGTCGCG 120
   |||||
DB 62 AGCTGAGCGGTGTATGTGGCGCAATACATGTCAACCCCGCTGCCGCAATGTCGCG 121
   |||||
QY 121 CCGCCCGGAAGCGCACCGCTGCGGCTGATTTCTCGATGATTTGGAGATGCTG----- 175
   |||||
DB 122 CCGCCCGGAAGCGCACCGCTGCGGCTGATTTCTCGATGATTTGGAGATGCTGCGCACG 181
   |||||
QY 176 ----- 175

```

Accession	Gene	Species	Strain	Position (bp)	Sequence	Length (bp)
D8	182	GA183GCGAAGACCTTTGCGACAGTATCAGAAAGTTCACATATTCACATATATATCTGCCCCGATG	241			
QY	176	-GCCCTGTAGACCTGTTATACATTTAAATATGAACGTGGCTATGCGCTTACATGGTTGATATTA	234			
D8	242	CGCCCTGTAGACCTGTTATACATTAATATGAACGTGGCTATGCGCTTACATGGTTGATATTA	301			
QY	235	TTGGGCTTTGACCGAATTTCCACAGGAGATGAATCTGGGATTTAAACAGGACGAGAAATA	294			
QY	295	TAAAGCTTTGATTTGATTCAGAAAGTGAAGATGGCATTCCTCTTCAACAGATTAATTTGG	354			
D8	362	TAAAGCTTTGATTTGATTCAGAAAGTGAAGATGGCATTCCTCTTCAACAGATTAATTTGG	421			
QY	355	GAGGTTTTTTCACAGGAGAGACCTTATCTTATATATCTGCCCTTACACACAGCAAAAC	414			
D8	422	GAGGTTTTTTCACAGGAGAGACCTTATCTTATATATCTGCCCTTACACACAGCAAAAC	481			
QY	415	TGGCAGAGTGTACTGCATCAGTTCTTGTGCTTCCACTTTCGGGNTTCCCTTTCACAGGGKC	474			
D8	482	TGGCAGAGTGTACTGCATCAGTTCTTGTGCTTCCACTTTCGGGNTTCCCTTTCACAGGGKC	541			
QY	475	CTATGCGTGTGTCTTAATAGAGATATTTCTATTTCTTCACAGTGCACAGGGGATTTGACCCCTT	534			
D8	542	CTATGCGTGTGTCTTAATAGAGATATTTCTATTTCTTCACAGTGCACAGGGGATTTGACCCCTT	601			
QY	535	TGTTTCCCTGATGTTGGTCTCTTACGGGTGGAAGAACTTAAACATTTGGTGAATCAG	594			
D8	602	TGTTTCCCTGATGTTGGTCTCTTACGGGTGGAAGAACTTAAACATTTGGTGAATCAG	661			
QY	595	CCAAATGTGACCTTTAAACCTATGAAAGGTATGATGCACAGTTCGTCTCAACAGAGAAATGA	654			
D8	662	CCAAATGTGACCTTTAAACCTATGAAAGGTATGATGCACAGTTCGTCTCAACAGAGAAATGA	721			
QY	655	TGAGTGTCAACCAATTCATTTATATACTCCATCTCCAATTTGATGTGACGTACATA	709			
D8	722	TGAGTGTCAACCAATTCATTTATATACTCCATCTCCAATTTGATGTGACGTACATA	776			
RESULT 4						
ABK37045						
ID	ABK37045	standard; cDNA; 1556 BP.				
XX	ABK37045;					
AC						
XX						
DT	08-MAY-2002	(first entry)				
XX						
DE		DNA encoding human lysophospholipase I #3.				
KW		Human; mouse; antiinflammatory; antiatherosclerotic; vasotropic;				
KW		antiinflammatory; cardiant; lysophospholipase I; inflammation; ischaemia;				
KW		hyperlipidaemia; cardiovascular disorder; atherosclerosis;				
KW		antisense gene therapy; gene; ss.				
OS		Homo sapiens.				
XX						
PN	WO200210185-A1.					
PD						
XX	07-FEB-2002.					
PF						
XX	20-JUL-2001; 2001WO-US22975.					
XX						
PR	31-JUL-2000; 2000US-0629645.					
XX						
PA	(ISIS-) ISIS PHARM INC.					
XX						
PI	Bennett CF, Wyatt JR;					
XX						
DR	WPI; 2002-188720/24.					
DR	P-PSDB; AAU85134.					
XX						
PT		Novel antisense compound useful for treating inflammation,				

PT	hyperlipidaemia, and cardiovascular disorders such as atherosclerosis
PT	and myocardial ischaemia, inhibits lysophospholipase I -
PS	Example 15; Page 95-96; 131pp: English.
XX	
XX	The invention relates to an antisense compound (I) 8-30 nucleobases in
CC	length targeted to a nucleic acid molecule encoding lysophospholipase I
CC	(II), where (I) specifically hybridises with and inhibits the expression
CC	of (II). (I) is useful for inhibiting the expression of (II) in cells or
CC	tissues, and for treating a human having a disease or condition
CC	associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
CC	and cardiovascular disorders such as atherosclerosis and myocardial
CC	ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
CC	useful for distinguishing functions of various members of a biological
CC	pathway. (I) is useful in antisense gene therapy. ABK37028-ABK37191
CC	represent lysophospholipase I coding sequences, antisense
CC	oligonucleotides and related PCR primers of the invention.
XX	
XX	Sequence 1556 BP; 423 A; 324 C; 350 G; 459 T; 0 other;
Query Match	88.6%; Score 628.4; DB 24; Length 1556;
Best Local Similarity	91.0%; Pred. No. 2.3e-190;
Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1.	
QY	1 GCCGCTGCACGCCCTTGGGCGCGCGCGCGCGCGCGCTCTTCCTTCGCGCTGCG 60
DB	121 GCCGCTGCACGCCCTTGGGCGCGCGCGCGCGCGCGCTCTTCGCGCTGCG 180
QY	61 AGCTAGGCGGTGATATGTCGCGCAATTAACATCTCAACCCCGTCCGCGCATCGTCCG 120
DB	181 AGCTAGGCGGTGATATGTCGCGCAATTAACATCTCAACCCCGTCCGCGCATCGTCCG 240
QY	121 CGCCCGGAAGGCCACCGCTGCGGTGATTTTCTCGATGATTTGGAGATCTGCG---- 175
DB	241 CGCCCGGAAGGCCACCGCTGCGGTGATTTTCTCGATGATTTGGAGATCTGCGCGACG 300
QY	176 ----- 175
DB	301 GATGGGCGAAGACCTTTCAGGTATCAGAACTTCAATCTCAAAATATATCTCCCGCANG 360
QY	176 -GCGTTAGAGCGCTGTACATTAAATATGACGTCGCTATGCGCTTCATGCTTGTATATTA 234
DB	361 GCGCTTTAGAGCGCTGTACATTAAATATGACGTCGCTATGCGCTTCATGCTTGTATATTA 420
QY	235 TTGGGCTTTCACCAATTCACAGAGGAGATGATTCGGGATTAAACAGCAGAGAAATTA 294
DB	421 TTGGGCTTTCACCAATTCACAGAGGAGATGATTCGGGATTAAACAGCAGAGAAATTA 480
QY	295 TAAAGCTTTGATGATCAAGAAGTGAAGAAATGGCATTCCTCTCTAACAAGATTTATTTGG 354
DB	481 TAAAGCTTTGATGATCAAGAAGTGAAGAAATGGCATTCCTCTCTAACAAGATTTATTTGG 540
QY	355 GAGGCTTTTCTAGAGGAGAGCTTATCTTTATATATCTGCCCTTACCAACAGCAGAAAC 414
DB	541 GAGGCTTTTCTAGAGGAGAGCTTATCTTTATATATCTGCCCTTACCAACAGCAGAAAC 600
QY	415 TGGCAGGTGTCACTCACTCACTCACTTCTTGCTTCCACTTGGGNTTCTCTTCCACAGGGKC 474
DB	601 TGGCAGGTGTCACTCACTCACTCACTTCTTGCTTCCACTTGGGNTTCTCTTCCACAGGGKC 660
QY	475 CTATCGGTGTGCTAATAGAGATTTTCTATTTCTCAAGTCCACGAGGGATTTGACCTTT 534
DB	661 CTATCGGTGTGCTAATAGAGATTTTCTATTTCTCAAGTCCACGAGGGATTTGACCTTT 720
QY	535 TGGTCCCTCGATGTTTGGTTCCTTAGCGGTGAAAACTAAAAACATTTGGATTCAG 594
DB	721 TGGTCCCTCGATGTTTGGTTCCTTAGCGGTGAAAACTAAAAACATTTGGATTCAG 780
QY	595 CCAATGTACCTTTAAACCTATGAGAGTATGATGACAGTTCGTTCAACAGAGAAATGA 654
DB	781 CCAATGTACCTTTAAACCTATGAGAGTATGATGACAGTTCGTTCAACAGAGAAATGA 840
QY	655 TGGATGTCAAGCAATTCATGATTAACCTCTTACCTCAATTCGATTTGACGTCACTA 709

PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PI Schlegel R, Endege WO, Monahan JE;
 XX WPI; 2001-662795/76.
 DR
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1: Page 4933; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SO Sequence 2600 BP; 796 A; 470 C; 482 G; 850 T; 2 other:
 Query Match 88.6%; Score 628.4; DB 23; Length 2600;
 Best Local Similarity 91.0%; Pred. No. 3.2e-190;
 Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;
 QY 1 GCGGCTGCGACGCGCTTGGGCGCGGCGCGCGCGCTTCCTTCGCTGGCGCTGG 60
 DB 89 GCGGCTGCGACGCGCTTGGGCGCGGCGCGCGCGCTTCCTTCGCTGGCGCTGG 148
 QY 61 AGCTGAGCGGCTATGTGGCGCAATACATGTCAACCCCGCTGCCCGCATGTGCCG 120
 DB 149 AGCTGAGCGGCTATGTGGCGCAATACATGTCAACCCCGCTGCCCGCATGTGCCG 208
 QY 121 CCGCGCGGAAGCGCACCGCTGCGGTATTTCTGTCATGGATTGGAGATCTGG----- 175
 DB 209 CCGCGCGGAAGCGCACCGCTGCGGTATTTCTGTCATGGATTGGAGATCTGGCGCAG 268
 QY 176 ----- 175
 DB 269 GATGGCAGACGCTTGGCAGGTATAGAACTTACATATCAAAATATATCTGCCCGCATG 328
 QY 176 -GCGTGTAGGCGCTGTACATTAATATGAAAGCTGCTATGCGCTTCAGTGGTTGATATTA 234
 DB 329 CGCGTGTAGGCGCTGTACATTAATATGAAAGCTGCTATGCGCTTCAGTGGTTGATATTA 388
 QY 235 TTGGGCTTTACACAGATTTCACAGAGAGATCTGGGATTAAACGCGACGAGAAATA 294
 DB 389 TTGGGCTTTACACAGATTTCACAGAGAGATCTGGGATTAAACGCGACGAGAAATA 448
 QY 295 TAAAGCTTTGATGATCAAGAGATGAAGATGGCATTCCTCTTACAGATTAATTTTGG 354
 DB 449 TAAAGCTTTGATGATCAAGAGATGAAGATGGCATTCCTCTTACAGATTAATTTTGG 508
 QY 355 GAGGTTTTCTCAGGAGAGACTTTATCTTATATACCTGCCCTTACACAGACAGAAAC 414
 DB 509 GAGGTTTTCTCAGGAGAGACTTTATCTTATATACCTGCCCTTACACAGACAGAAAC 568
 QY 415 TGGCAGGTGTCATGCACTAGTTTCTGCTTCCACTTGGGATTCCTTTCCACAGAGGAC 474
 DB 569 TGGCAGGTGTCATGCACTAGTTTCTGCTTCCACTTGGGATTCCTTTCCACAGAGGAC 628

QY 475 CTATCGGNGGCTAATAGAGATATTCTATTCCTCAGTGCACGCGGATTTGACCTT 534
 DB 629 CTATCGGNGGCTAATAGAGATATTCTATTCCTCAGTGCACGCGGATTTGACCTT 688
 QY 535 TGGTCCCGCTGATGTTGGTCTCTTCTTACGGTGAAGAAACATTAATGTTGATTCAG 594
 DB 689 TGGTCCCGCTGATGTTGGTCTCTTCTTACGGTGAAGAAACATTAATGTTGATTCAG 748
 QY 595 CCAATGTACCTTTAAACCTATGAGTATGATGACACAGTCTGTCACAGGAATGA 654
 DB 749 CCAATGTACCTTTAAACCTATGAGTATGATGACACAGTCTGTCACAGGAATGA 808
 QY 655 TGGATGTCACCAATTCATGATTAACCTCTACCTCCAAATGATTGACGTCACTA 709
 DB 809 TGGATGTCACCAATTCATGATTAACCTCTACCTCCAAATGATTGACGTCACTA 863
 RESULT 7
 ID AAS71464 standard; cDNA; 1538 BP.
 XX AAS71464:
 AC AAS71464:
 XX 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #7268.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 XX 23-AUG-2000; 2000US-0649167.
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 DR WPI: 2001-639362/73.
 P-PSDB: ABG07277.
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 1: SEQ ID NO 7268; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridization probes,
 XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 XX and gene mapping, and in recombinant production of (II). The
 XX polynucleotides are also used in diagnostics as expressed sequence tags
 XX for identifying expressed genes. (I) is useful in gene therapy techniques
 XX to restore normal activity of (II) or to treat disease states involving
 XX (II). (II) is useful for generating antibodies against it, detecting or
 XX quantitating a polypeptide in tissue, as molecular weight markers and as
 XX a food supplement. (II) and its binding partners are useful in medical
 XX imaging of sites expressing (II). (I) and (II) are useful for treating
 XX disorders involving aberrant protein expression or biological activity.
 XX The polypeptide and polynucleotide sequences have applications in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits to assess biodiversity
 XX and to produce other types of data and products dependent on DNA and
 XX amino acid sequences. AAS64197-AAS94564 represent novel human
 XX diagnostic coding sequences of the invention.


```

Db      1  CCGGGCCCGGCTCTCTCCCTTCGCTTGAGCTGAGCGGCTGTATGTCGGCAAT 60
QY      87  AACATGCAACCCGGTGGCCGCGCATGTGCGCCGCCCGGAAGGCCACCGCTGCGGT 146
Db      61  AACATGCAACCCGGTGGCCGCGCATGTGCGCCGCCCGGAAGGCCACCGCTGCGGT 120
QY      147  ATTTTCCGATGATGGAGATGAGTCTG----- 175
Db      121  ATTTTCCGATGATGGAGATGAGTCTGCGCCGCGCATGTGCGCCGCCCGGAAGGCCACCGCTGCGGT 180
QY      176  -----GCTGTAGGCGCTTACATTAAT 200
Db      181  AGAGTTCATATCAATATATCTGCCGATGCGCTGTAGGCGCTTACATTAAT 240
QY      201  ATGACGCGGATGCGCTTCAATGATTTATTTGGGCTTTCACAGATTCACAGAG 260
Db      241  ATGACGCGGATGCGCTTCAATGATTTATTTGGGCTTTCACAGATTCACAGAG 300
QY      261  GATGATCTGGATTTAAACAGGACAGAAATATAAAGCTTTGATTCAGAAAGTG 320
Db      301  GATGATCTGGATTTAAACAGGACAGAAATATAAAGCTTTGATTCAGAAAGTG 360
QY      321  AAGATGCGATCTCTTCAACAGATTTATTTGGGAGGTTTTCACAGGAGGCTT 380
Db      361  AAGATGCGATCTCTTCAACAGATTTATTTGGGAGGTTTTCACAGGAGGCTT 420
QY      381  TCTTATATCTGCGCTTCAACAGAGAACTGGCAGGTGCTACTGCACTGATTC 440
Db      421  TCTTATATCTGCGCTTCAACAGAGAACTGGCAGGTGCTACTGCACTGATTC 480
QY      441  TTGCTTCCACTGCGGNTCTTTCACAGGAGGCTTATCGGTGCTATATAGATAT 500
Db      481  TGGCTTCCACTGCGGNTCTTTCACAGGAGGCTTATCGGTGCTATATAGATAT 540
QY      501  TCTATCTCAAGTCCAGCGGATTTGATGCTTGGTGGTGGTGGTGGTGGTGGT 560
Db      541  TCTATCTCAAGTCCAGCGGATTTGATGCTTGGTGGTGGTGGTGGTGGTGGT 600
QY      561  ACGGTGGAATACTAAACATTTGATGATCCAGCAATGTGACCTTTAAACCTATGA 620
Db      601  ACGGTGGAATACTAAACATTTGATGATCCAGCAATGTGACCTTTAAACCTATGA 660
QY      621  GGTATGATGACAGTTCGTGCAACAGAAATGATGATGTCACAGATTCATTTATA 680
Db      661  GGTATGATGACAGTTCGTGCAACAGAAATGATGATGTCACAGATTCATTTATA 720
QY      681  CTCCTACCTCCATTTGATGAGTCACTA 709
Db      721  CTCCTACCTCCATTTGATGAGTCACTA 749

```

RESULT 9
AAS56597
ID AAS56597 standard; cDNA: 2417 BP.

AC AAS56597;
XX 18-DEC-2001 (first entry)
XX
DE Human cDNA for an ovarian cancer protein #221.
XX
KW Human; ss: ovarian cancer protein; cancer; tumour; ovarian cancer;
KW endometrial cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200170976-A2.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US09062.
XX
PR 21-MAR-2000; 2000US-190710P.

```

PR      22-JUN-2000; 2000US-213748P.  
PR      19-DEC-2000; 2000US-257276P.  
PA      (CORI-) CORIXA CORP.  
PI      Xu J, Pyle RA, Stolk JA;  
XX      WPI; 2001-607531/69.  
DR      Nucleic acids encoding 222 polypeptides associated with ovarian and  
XX      endometrial cancers, useful for diagnosing, preventing and treating  
PT      cancers -  
PS      Claim 1; Page 186-187; 187pp; English.  
CC      The invention relates to human polynucleotides encoding proteins  
CC      associated with ovarian and endometrial cancers. The polynucleotides and  
CC      the proteins they encode may be used in the prevention, diagnosis and  
CC      treatment of diseases associated with the inappropriate expression of  
CC      ovarian and endometrial cancer polypeptides (OECPS). For example, the  
CC      polynucleotide (or an expression vector comprising the polynucleotide)  
CC      and the OECPS may be used to treat disorders associated with decreased  
CC      expression by rectifying mutations or deletions in a patient's genome  
CC      that affect the activity of OECPS by expressing inactive proteins or to  
CC      supplement the patients own production of them. Additionally, the  
CC      polynucleotide may be used to produce the OECPS, by inserting the nucleic  
CC      acids into a host cell and culturing the cell to express the protein. The  
CC      polynucleotide and its complementary sequences may also be used as DNA  
CC      probes in diagnostic assays to detect and quantitate the presence of  
CC      similar nucleic acids in samples, and therefore which patients may be in  
CC      need of restorative therapy. The OECPS may also be used as antigens in  
CC      the production of anti-OECPS antibodies and in assays to identify  
CC      modulators of its expression and activity. The anti-OECPS antibodies and  
CC      antagonists may also be used to down regulate expression and activity.  
CC      The anti-OECPS antibodies may also be used as diagnostic agents for  
CC      detecting the presence of OECPS in samples (e.g. by enzyme linked  
CC      immunosorbant assay (ELISA)) and hence diagnose patients with  
CC      cancers. The present sequence is a ovarian and endometrial cancer linked  
CC      cDNA of the invention.  
XX  
SQ      Sequence 2417 BP; 752 A; 414 C; 422 G; 829 T; 0 other;  
XX  
Query Match      83.1%; Score 589.4; DB 22; Length 2417;  
Best Local Similarity 90.5%; Pred. No. 9,5e-178;  
Matches 666; Conservative 1; Mismatches 66; Gaps 1;  
QY      40  CTTCCTCCGCTTGGCTGTAGCTGAGCGCGTGTATGTCGGCAATATCAATCAACC 99  
Db      1  CTTCCTCCGCTTGGCTGTAGCTGAGCGCGTGTATGTCGGCAATATCAATCAACC 60  
QY      100 CGCTGCGCGCATGCTGCGCGCGCGCGCGAGGACCGCTGCGGTATTTCTGCGATG 159  
Db      61  CGCTGCGCGCATGCTGCGCGCGCGCGCGAGGACCGCGCTGCGGTATTTCTGCGATG 120  
QY      160 GATGAGGATGAGTCTG----- 175  
Db      121 GATGAGGATGAGTCTGCGAGATGGCAGAGCTTTCAGATATCAAGATTCACATA 180  
QY      176 -----GCTGTAGGCGCTTACATTAATTTGAAGCGGCTA 213  
Db      181 TCAATATATCTGCCGATGCGCTGTAGGCGCTTACATTAATTTGAAGCGGCTA 240  
QY      214 TCCCTTCAATGCTTATATTTATGCGCTTTCACAGATTCACAGAGGATGATCTGGA 273  
Db      241 TCCCTTCAATGCTTATATTTATGCGCTTTCACAGATTCACAGAGGATGATCTGGA 300  
QY      274 TTAACAGGACAGAAATATTAAGCTTTGATTCAGAAAGTGAAGATGCGATTC 333  
Db      301 TTAACAGGACAGAAATATTAAGCTTTGATTCAGAAAGTGAAGATGCGATTC 360  
QY      334 CTCTTCAAGATTTATTTGGAGGTTTTCAGAGGAGGCTTATCTTATATCTG 393  
Db      361 CTCTTCAAGATTTATTTGGAGGTTTTCAGAGGAGGCTTATCTTATATCTG 420

```

the array comprises nucleic acid polymers which are specific for less

DE DNA encoding human lysophospholipase I #1.

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
 KW antilipemic; cardiant; lysophospholipase I; inflammation; ischaemia;
 KM hyperlipidaemia; cardiovascular disorder; atherosclerosis;
 KW antisense gene therapy; gene; ss.
 OS Homo sapiens.
 PN WO200210185-A1.
 XX 07-FEB-2002.
 PD 20-JUL-2001; 2001WO-US22975.
 PF 31-JUL-2000; 2000US-0629645.
 PR (ISIS-) ISIS PHARM INC.
 PA Bennett CF, Wyatt JR;
 PI WPI; 2002-188720/24.
 DR P-PSDB; AAU85132.
 XX Novel antisense compound useful for treating inflammation,
 PT hyperlipidaemia, and cardiovascular disorders such as atherosclerosis
 PT and myocardial ischaemia, inhibits lysophospholipase I -
 PS Example 13; Page 88-90; 131pp; English.
 XX The invention relates to an antisense compound (I) 8-30 nucleobases in
 CC length targeted to a nucleic acid molecule encoding lysophospholipase I
 CC (II), where (I) specifically hybridises with and inhibits the expression
 CC of (II). (I) is useful for inhibiting the expression of (II) in cells or
 CC tissues, and for treating a human having a disease or condition
 CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
 CC and cardiovascular disorders such as atherosclerosis and myocardial
 CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway. (I) is useful in antisense gene therapy. ABK37028-ABK37191
 CC represent lysophospholipase I coding sequences, antisense
 CC oligonucleotides and related PCR primers of the invention.
 XX Sequence 2417 BP; 752 A; 414 C; 422 G; 829 T; 0 other;
 SQ
 Query Match 83.1%; Score 589.4; DB 24; Length 2417;
 Best Local Similarity 90.5%; Pred. No. 9.5e-178;
 Matches 666; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

DB 361 CTTCTAACAGATTATTTGGAGGTTTCTCAGGAGGAGCTTATCTTATATACTG 420
 QY 394 CCCTTACACACAGAGAAATGCGAGGTGCTACTGCTAGTTCTTGGTTCACATC 453
 DB 421 CCCTTACACACAGAGAAATGCGAGGTGCTACTGCTAGTTCTTGGTTCACATC 480
 QY 454 GGGNTTCCCTTCCACAGGKCCATCGGGTGGTAAATAGAAATATCTTATCTCCAGT 513
 DB 481 GGGCTTCTTCCACAGGCTCTATCGGGTGGTAAATAGAAATATCTTATCTCCAGT 540
 QY 514 GCCACGGAGATGTGACCTTTGGTCCCTGATGTTGGTTCCTTACGCTGAAAAAC 573
 DB 541 GCCACGGAGATGTGACCTTTGGTCCCTGATGTTGGTTCCTTACGCTGAAAAAC 600
 QY 574 TAAACATTTGTGATTCACGCAATGTGACCTTTAAACCTATAGAGTATGATGCA 633
 DB 601 TAAACATTTGTGATTCACGCAATGTGACCTTTAAACCTATAGAGTATGATGCA 660
 QY 634 GTTCGTGTCACAGGAATGATGATGTCACCAATTCATTTGATTAACCTCTACCTCCA 693
 DB 661 GTTCGTGTCACAGGAATGATGATGTCACCAATTCATTTGATTAACCTCTACCTCCA 720
 QY 694 TTGATTGACGTCACTA 709
 DB 721 TTGATTGACGTCACTA 736
 RESULT 12
 AAZ61501
 ID AAZ61501 standard; cDNA; 1300 BP.
 XX
 AC AAZ61501;
 DT 19-UDN-2000 (first entry)
 XX
 DE cDNA encoding a human lysophospholipase protein designated CBFLH05.
 XX
 KW Human; lysophospholipase; CBFLH05; liver disease; cancer;
 KW autoimmune disease; kidney disorder; vaccine; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 6..650
 FT /*tag= a
 FT /product= "lysophospholipase"
 XX
 PN WO200009556-A1.
 XX
 PD 24-FEB-2000.
 PF 11-AUG-1998; 98WO-CN00164.
 PR 11-AUG-1998; 98WO-CN00164.
 XX
 PA (UYSH-) UNIV SHANGHAI SECOND MEDICAL.
 PI Zhou J, Mao M, Ye M, Zhang Q;
 DR WPI; 2000-224281/19.
 DR P-PSDB; AA169296.
 XX
 PT New human lysophospholipase gene (designated CBFLH05) polypeptides and
 PT polynucleotides used to identify agonists, antagonists and inhibitors
 PT for use in (gene) therapy -
 PS Claim 1; Page 22-23; 36pp; English.
 XX The present sequence encodes a human lysophospholipase protein
 CC (designated CBFLH05). CBFLH05 polypeptides may be used for
 CC identifying agonists and antagonists/inhibitors, and for detecting
 CC and treating diseases associated with inappropriate CBFLH05 activity

CC or levels. CBRBLH05 polypeptides and polynucleotides, agonists,
CC antagonists and antibodies are used for the treatment of liver diseases,
CC cancer, autoimmune diseases, and kidney disorders. The polynucleotide
CC is also useful as a source of primers and probes, and also for detecting
CC the above diseases. The polypeptide may also be used as a vaccine.

XX Sequence 1300 BP; 381 A; 246 C; 254 G; 419 T; 0 other;

Query Match 79.1%; Score 561; DB 21; Length 1300;
Best Local Similarity 92.2%; Pred. No. 8,2e-169;
Matches 607; Conservative 1; Mismatches 32; Indels 18; Gaps 1;

```

OY 70 GGTGATGCGCGCAATACATGTCACCCGCGCCGCGCATCGTCCGCCGCCGCGCA 129
    |||||
DB 1 GGTGATGCGCGCAATACATGTCACCCGCGCCGCGCATCGTCCGCCGCCGCGCA 60
OY 130 AGCCACCGCTGCGGATTTTCCGTCATGATTTGGGATACCTGCGCTTACGCTG 189
    |||||
DB 61 AGCCACCGCTGCGGATTTTCCGTCATGATTTGGGATACCTGCGCTTACGCTG 120
OY 190 TTACATT-----AAATATGAACGTGGCTATGCTTCATGGTTTGATA 231
    |||||
DB 121 AAGCCTTTCAGAGTATCAGAACTTCAATCAATATATCTGCCCGATCGTTTGATA 180
OY 232 TTATTGGGCTTTCACACAGATTCACAGAGATGTAATCGGATTAACAGCAGCAGAAA 291
    |||||
DB 181 TTATTGGGCTTTCACACAGATTCACAGAGATGTAATCGGATTAACAGCAGCAGAAA 240
OY 292 ATATATAAGCTTTGATGATATCAAGAAGGAAGATGCGATTCCTTTACAGAAATTTT 351
    |||||
DB 241 ATATATAAGCTTTGATGATATCAAGAAGGAAGATGCGATTCCTTTACAGAAATTTT 300
OY 352 TGGGAGGCTTTTCAGAGGAGAGCTTATCTTATATACAGCCCTTACACAGAGAGA 411
    |||||
DB 301 TGGGAGGCTTTTCAGAGGAGAGCTTATCTTATATACAGCCCTTACACAGAGAGA 360
OY 412 AACTGGCAGGTGTCACCTCAGCTTCTTGCCTTCACCTCGGAGNTTCTTTCCACAGG 471
    |||||
DB 361 AACTGGCAGGTGTCACCTCAGCTTCTTGCCTTCACCTCGGAGNTTCTTTCCACAGG 420
OY 472 GKCCTATGGGTGCTAATAGAGATTTTCTATTTCTCAATGCCACAGGAGATTGTGAC 531
    |||||
DB 421 GTCCTATGGGTGCTAATAGAGATTTTCTATTTCTCAATGCCACAGGAGATTGTGAC 480
OY 532 CTTTGGTCCCTGATGTTTGGTCTCTTACGTTGAGAAAACCTAATAACATTGGTGAATC 591
    |||||
DB 481 CTTTGGTCCCTGATGTTTGGTCTCTTACGTTGAGAAAACCTAATAACATTGGTGAATC 540
OY 592 CAGCCAAATGTACCTTTAAACCTATGAAGGTATGATGACAGATTCGTGTCAACAGAAA 651
    |||||
DB 541 CAGCCAAATGTACCTTTAAACCTATGAAGGTATGATGACAGATTCGTGTCAACAGAAA 600
OY 652 TGATGAGATGTACAGCAATTCATGATAACTCTCACTCCATTTGATTGACGTCACTA 709
    |||||
DB 601 TGATGAGATGTACAGCAATTCATGATAACTCTCACTCCATTTGATTGACGTCACTA 658

```

RESULT 13

ABK37037
ID ABK37037 standard; cDNA: 693 BP.

XX ABR37037;

XX 08-MAY-2002 (first entry)

XX DNA encoding mouse lysophospholipase I #1.

XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;
XX antiinflammatory; cardiant; lysophospholipase I; inflammation; ischaemia;
XX hyperlipidaemia; cardiovascular disorder; atherosclerosis;
XX antisense gene therapy; gene; ss.

OS Mus sp.

```

XX XX
PN W0200210185-A1.
XX 07-FEB-2002.
PD
XX
XX 20-JUL-2001; 2001WO-US22975.
XX
XX 31-JUL-2000; 2000US-0629645.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Wyatt JR.
XX
XX WPI; 2002-188720/24.
XX
XX P-PSDB; AA085133.
XX
XX Novel antisense compound useful for treating inflammation,
XX hyperlipidaemia, and cardiovascular disorders such as atherosclerosis
XX and myocardial ischaemia, inhibits lysophospholipase I -
XX
XX Example 13; Page 92-93; 131pp; English.
XX
XX
XX The invention relates to an antisense compound (I) 8-30 nucleobases in
XX length targeted to a nucleic acid molecule encoding lysophospholipase I
XX (II), where (I) specifically hybridises with and inhibits the expression
XX of (II). (I) is useful for inhibiting the expression of (II) in cells or
XX tissues, and for treating a human having a disease or condition
XX associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,
XX and cardiovascular disorders such as atherosclerosis and myocardial
XX ischaemia. (I) is useful as research reagent and diagnostics. (I) is also
XX useful for distinguishing functions of various members of a biological
XX pathway. (I) is useful in antisense gene therapy. ABK37028-ABK37191
XX represent lysophospholipase I coding sequences, antisense
XX oligonucleotides and related PCR primers of the invention.
XX
XX
XX Sequence 693 BP; 181 A; 168 C; 158 G; 186 T; 0 other;

```

Query Match 61.5%; Score 436; DB 24; Length 693;
Best Local Similarity 79.9%; Pred. No. 6.1e-129;
Matches 554; Conservative 1; Mismatches 72; Indels 66; Gaps 1;

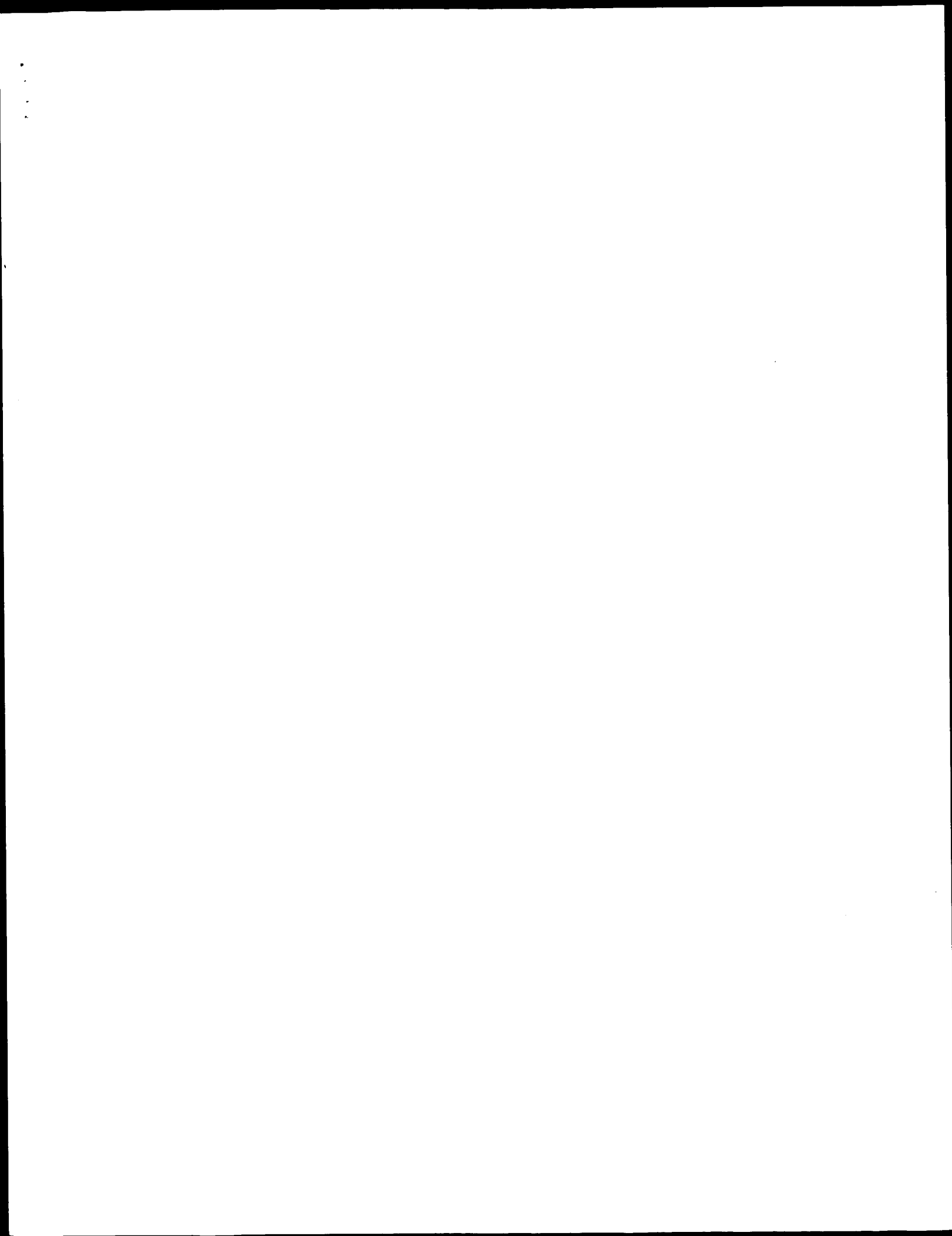
```

OY 75 ATGTGCGGCAATACATGTCACCCGCGCTGCCCATCGTCCGCCGCCGCGGAAGGCC 134
    |||||
DB 1 ATGTGCGGCAATACATGTCACCCGCGCTGCCCATCGTCCGCCGCCGCGGAAGGCC 60
OY 135 ACCGCTCGGTGATTTTCTCGCATGATTTGGGATACCTGCGG-----176
    |||||
DB 61 ACCGCTCGGTGATTTTCTCGCATGATTTGGGATACCTGCGG-----176
OY 177 -----CCTGTTAGGCTT 188
    |||||
DB 121 TTTCAGAGTATCAAAAGTCCCAATCAATATACATCTGTCACATCCCTGTGATGCA 180
OY 189 GTTACATTAAATATGAACGTCATGCTTACATGTTGATTTATTTGGGCTTTTCACCA 248
    |||||
DB 181 GTTACATTAAATATGAACGTCATGCTTACATGTTGATTTATTTGGGCTTTTCACCA 240
OY 249 GATTACAGAGAGATGATTTGGGATTAACAGCAGCAGCAAGAAATATTAAGCTTTGATT 308
    |||||
DB 241 GATTCCAGAGAGATGATTTGGGATTAACAGCAGCAGCAAGAAATATTAAGCTTTGATT 300
OY 309 GATTCAGAAAGTGAAGATGATTCCTTCATCAAGAAATATTTTGGAGAGGTTTCTCAG 368
    |||||
DB 301 GATTCAGAAAGTGAAGATGATTCCTTCATCAAGAAATATTTTGGAGAGGTTTCTCAG 360
OY 369 GGAGAGCTTATCTTATATACCTGCTTACACACAGCAGCAAGAACTGCGAGTGTCACT 428
    |||||
DB 361 GGAGAGCTTATCTTATATACCTGCTTACACACAGCAGCAAGAACTGCGAGTGTCACT 420
OY 429 GCACCTAGTTTCTGCTTCACCTCGGAGTCTTTCCACAGGAGGCTTATCGTGGTGTCT 488
    |||||
DB 421 GCACCTAGTTTCTGCTTCACCTCGGAGTCTTTCCACAGGAGGCTTATCGTGGTGTCT 480

```


XX (CORI-) CORIXA CORP.
XX
XX Jiang Y, Harlocker SL, Secret H;
XX
XX WPI; 2002-114514/15.
XX
XX Novel isolated colon tumor polynucleotide differentially expressed in
XX colon tumor or colon metastatic tumor and polypeptides encoded by them,
XX useful for inhibiting development of cancer in patient -
XX
XX Claim 1; SEQ ID 1369; 105bp; English.
XX
XX ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I)
XX which were isolated from human colon tumour and colon metastatic tumour
XX cDNA libraries. (I) have cytostatic activity and can be used in vaccine
XX production. (I) can be used for stimulating and/or expanding T cells
XX specific for a tumour protein on contact with the T cells. They are also
XX useful for inhibiting the development of cancer in a patient. (I) can be
XX used as probes or primers for nucleic acid hybridisation, for preparing
XX mutant species primers, or primers for use in genetic constructions. (I)
XX can be used in the diagnosis of a colon tumour.
XX
XX Sequence 419 BP; 125 A; 95 C; 88 G; 109 T; 2 other;
XX
XX Query Match 55.4%; Score 392.6; DB 24; Length 419;
XX Best Local Similarity 98.7%; Pred. No. 3.6e-115;
XX Matches 393; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
OY 312 CAAGAGTGAAGATGGCTTCCTCTTAACAGATTTATTTGGAGGTTTCTCAGGGA 371
DB :|||||
DB 417 HAAGAGTGAAGATGGCTTCCTCTTAACAGATTTATTTGGAGGTTTCTCAGGGA 358
OY 372 GGAGCTTTATCTTTATATCTGCTTACACAGAGGAATGGAGGTGTCTACTCA 431
DB :|||||
DB 357 GGAGCTTTATCTTTATATCTGCTTACACAGAGGAATGGAGGTGTCTACTCA 298
OY 432 CTCAGTTCTGCTTCCACTTGGGNTTCCTTCCACAGAGGKCTATCGTGTCTAAT 491
DB :|||||
DB 297 CTCAGTTCTGCTTCCACTTGGGNTTCCTTCCACAGAGGKCTATCGTGTCTAAT 238
OY 492 AAGATATTTCTATCTCAGTGCACGCGGATTTGACCCCTTGGTCCCGTGAATGTTT 551
DB :|||||
DB 237 AAGATATTTCTATCTCAGTGCACGCGGATTTGACCCCTTGGTCCCGTGAATGTTT 178
OY 552 GGTTCTTAGAGTGAAGAACTAATAACATGATGATCCAGCAATGTGACCTTAA 611
DB :|||||
DB 177 GGTTCTTAGAGTGAAGAACTAATAACATGATGATCCAGCAATGTGACCTTAA 118
OY 612 ACCATGAAGTATGATGACAGTTCGTCAACAGAAATGATGATGTCAGCAATTC 671
DB :|||||
DB 117 ACCATGAAGTATGATGACAGTTCGTCAACAGAAATGATGATGTCAGCAATTC 58
OY 672 ATTGATTAACCTCTACCTCCATTTGATGACGTCACTA 709
DB :|||||
DB 57 ATTGATTAACCTCTACCTCCATTTGATGACGTCACTA 20

Search completed: January 19, 2003, 01:43:02
Job time : 307 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2003, 01:35:50 ; Search time 70 Seconds
(without alignments)
3106.197 Million cell updates/sec

Title: US-09-988-982-2

Perfect score: 709
Sequence: 1 GCCGCTCGACAGCCCTTGCG.....CCATTGATTGACTACTA 709

Scoring table:
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Issued_patents_NA.*
2: /cgn2_6/ptodata/2/1na/5A.COMB.seq.*
3: /cgn2_6/ptodata/2/1na/5B.COMB.seq.*
4: /cgn2_6/ptodata/2/1na/6A.COMB.seq.*
5: /cgn2_6/ptodata/2/1na/6B.COMB.seq.*
6: /cgn2_6/ptodata/2/1na/PTCUS.COMB.seq.*
7: /cgn2_6/ptodata/2/1na/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	707.6	99.8	709	2	US-08-844-120-2
2	707.6	99.8	709	2	US-09-022-940-2
3	707.6	99.8	709	3	US-09-216-386-2
4	707.6	99.8	709	4	US-09-213-394-2
5	628.4	88.6	1486	2	US-09-022-940-4
6	628.4	88.6	1486	3	US-09-216-386-4
7	628.4	88.6	1556	4	US-09-629-645A-18
8	589.4	83.1	2417	4	US-09-629-645A-3
9	436	61.5	693	4	US-09-629-645A-10
10	433.2	61.1	727	4	US-09-629-645A-21
11	217.2	30.6	1624	3	US-09-013-881-15
12	90.6	12.8	608	4	US-09-629-645A-20
13	55.8	7.9	975	3	US-09-216-001-2
14	55.8	7.9	975	3	US-08-878-862-2
15	33.8	4.8	1356	4	US-09-371-913A-8
16	33	4.7	12001	1	US-08-458-568A-11
17	32.8	4.6	6216	3	US-09-213-053-1
18	32.2	4.5	1080	4	US-09-324-910-11
19	32	4.5	32	4	US-09-629-645A-6
20	31.8	4.5	5407	4	US-09-453-702B-201
21	31.4	4.4	4257	2	US-08-690-473-1
22	31.4	4.4	4257	4	US-09-259-821A-1
23	31.4	4.4	4257	4	US-08-843-659-1
24	31.4	4.4	4403765	4	US-09-103-840A-2
25	31.4	4.4	4411529	4	US-09-103-840A-1
26	31.2	4.4	2923	6	5187076-5
27	31	4.4	364	1	US-08-620-467A-11

28	31	4.4	364	1	US-08-348-572-11	Sequence 11, Appl
29	31	4.4	364	3	US-09-041-090B-11	Sequence 11, Appl
30	31	4.4	2673	4	US-09-336-447A-12	Sequence 12, Appl
31	30.8	4.3	418	3	US-09-141-000-6	Sequence 6, Appl
32	30.8	4.3	458	3	US-09-141-000-4	Sequence 4, Appl
33	30.8	4.3	481	4	US-09-116-492A-3	Sequence 3, Appl
34	30.8	4.3	524	4	US-09-116-492A-2	Sequence 2, Appl
35	30.8	4.3	855	4	US-09-116-492A-36	Sequence 36, Appl
36	30.8	4.3	1069	4	US-09-116-492A-37	Sequence 37, Appl
37	30.8	4.3	1277	4	US-09-116-492A-1	Sequence 1, Appl
38	30.8	4.3	1282	4	US-09-116-492A-38	Sequence 38, Appl
39	30.8	4.3	1317	4	US-09-172-952-5	Sequence 5, Appl
40	30.8	4.3	1616	4	US-08-818-112-112	Sequence 112, App
41	30.8	4.3	1616	4	US-08-818-111-107	Sequence 107, App
42	30.8	4.3	1616	4	US-09-056-556-112	Sequence 112, App
43	30.8	4.3	1616	4	US-09-072-596-107	Sequence 107, App
44	30.8	4.3	2060	4	US-09-370-807-1	Sequence 1, Appl
45	30.8	4.3	2060	4	US-09-921-259-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-844-120-2
Sequence 2, Application US/08844120
Patent No. 5858756
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPlicant: Shah, Purvi
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOT19
CLONE: 2676650
US-08-844-120-2
Query Match 99.8%; Score 707.6; DB 2; Length 709;
Best Local Similarity 100.0%; Pred. No. 4.3e-226;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCGCTCGACAGCCCTTGCGCGCGCGCGCGCGCGCTTCCTTCGCTGCGCTGCG 60
DB 1 GCCGCTCGACAGCCCTTGCGCGCGCGCGCGCGCGCTTCCTTCGCTGCGCTGCG 60

```

QY 61 AGCTGAGCGGCTGTATGTCCGCAATACATGTCAACCCCGCTGCCGCAATCGTCCCG 120
    |||
    |||
    |||
Db 61 AGCTGAGCGGCTGTATGTCCGCAATACATGTCAACCCCGCTGCCGCAATCGTCCCG 120
QY 121 CGGCCCGGAAGGCGACCGCTGGGCGATTTCTCGCATGATGGAGATCTAGTGGCGCTG 180
    |||
    |||
    |||
Db 121 CGGCCCGGAAGGCGACCGCTGGGCGATTTCTCGCATGATGGAGATCTAGTGGCGCTG 180
QY 181 TTAGGCGCTGTACATTAATATGACGTGGCTATGCGCTTCATGTTGATTTATTTGGGC 240
    |||
    |||
    |||
Db 181 TTAGGCGCTGTACATTAATATGACGTGGCTATGCGCTTCATGTTGATTTATTTGGGC 240
QY 241 TTTCACCAATTCACAGGAGGATGATGCGATTAACAGGACAGAGAAATATTAAG 300
    |||
    |||
    |||
Db 241 TTTCACCAATTCACAGGAGGATGATGCGATTAACAGGACAGAGAAATATTAAG 300
QY 301 CTTTGATGATCAAGAGGAGATGCGATTCCTTCTAACAGAAATTTATTTGGAGGCT 360
    |||
    |||
    |||
Db 301 CTTTGATGATCAAGAGGAGATGCGATTCCTTCTAACAGAAATTTATTTGGAGGCT 360
QY 361 TTTCAGGAGGAGCTTTATCTTTATTAATGCTCCCTTACACACAGCAGAACTGGCAG 420
    |||
    |||
    |||
Db 361 TTTCAGGAGGAGCTTTATCTTTATTAATGCTCCCTTACACACAGCAGAACTGGCAG 420
QY 421 GTGTACAGCTGACATGTTCTTCTCCACTTCGCGGNTCCCTTCCACAGGKCCATG 480
    |||
    |||
    |||
Db 421 GTGTACAGCTGACATGTTCTTCTCCACTTCGCGGNTCCCTTCCACAGGKCCATG 480
QY 481 GTGTCTAATAGATATTTCTATTTCTCAGTGCACGCGGATTTGTCACCTTTGGTTC 540
    |||
    |||
    |||
Db 481 GTGTCTAATAGATATTTCTATTTCTCAGTGCACGCGGATTTGTCACCTTTGGTTC 540
QY 541 CCTGATGTTGGTCTCTTACGCTGGAAGAACTAAACATTTGGTGAATCCAGCCATG 600
    |||
    |||
    |||
Db 541 CCTGATGTTGGTCTCTTACGCTGGAAGAACTAAACATTTGGTGAATCCAGCCATG 600
QY 601 TGACCTTTAAACCTATGAGATGATGATGACAGCTTCGCTCAACAGGAATGATGATG 660
    |||
    |||
    |||
Db 601 TGACCTTTAAACCTATGAGATGATGATGACAGCTTCGCTCAACAGGAATGATGATG 660
QY 661 TCAAGCAATTCATGATTAACCTCTACCTCAATGATGATGACGCTACTA 709
    |||
    |||
    |||
Db 661 TCAAGCAATTCATGATTAACCTCTACCTCAATGATGATGACGCTACTA 709

RESULT 2
US-09-022-940-2
; Sequence 2, Application US/09022940
; Patent No. 5965423
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: HUMAN LYOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,940
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-022-940-2

Query Match      99.8%; Score 707.6; DB 2; Length 709;
Best Local Similarity 100.0%; Pred. No. 4, 3e-226;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTCGACGCGCTTGGGCGGCGGCGGCGGCGCTTCTCCGCTTGGCTGTG 60
    |||
    |||
    |||
Db 1 GCGGCTCGACGCGCTTGGGCGGCGGCGGCGGCGGCGCTTCTCCGCTTGGCTGTG 60
QY 61 AGCTGAGCGGCTGTATGTGCGGCAATAATGTCACACCCGCTGCCCATGCTGCCG 120
    |||
    |||
    |||
Db 61 AGCTGAGCGGCTGTATGTGCGGCAATAATGTCACACCCGCTGCCCATGCTGCCG 120
QY 121 CGGCCCGGAAGGCGACCGCTGGGCGATTTCTCGCATGATGGAGATCTAGTGGCGCTG 180
    |||
    |||
    |||
Db 121 CGGCCCGGAAGGCGACCGCTGGGCGATTTCTCGCATGATGGAGATCTAGTGGCGCTG 180
QY 181 TTAGGCGCTGTACATTAATATGAACTGCTATGCTTCACTGTTGATTTATTTGGGC 240
    |||
    |||
    |||
Db 181 TTAGGCGCTGTACATTAATATGAACTGCTATGCTTCACTGTTGATTTATTTGGGC 240
QY 241 TTTCACCAATTCACAGGAGGATGATGCGATTAACAGGACAGCAGAAATATTAAG 300
    |||
    |||
    |||
Db 241 TTTCACCAATTCACAGGAGGATGATGCGATTAACAGGACAGCAGAAATATTAAG 300
QY 301 CTTTGATGATCAAGAGGAGATGCGATTCCTTCTAACAGAAATTTATTTGGAGGCT 360
    |||
    |||
    |||
Db 301 CTTTGATGATCAAGAGGAGATGCGATTCCTTCTAACAGAAATTTATTTGGAGGCT 360
QY 361 TTTCAGGAGGAGCTTTATCTTTATTAATGCTCCCTTACACACAGCAGAACTGGCAG 420
    |||
    |||
    |||
Db 361 TTTCAGGAGGAGCTTTATCTTTATTAATGCTCCCTTACACACAGCAGAACTGGCAG 420
QY 421 GTGTACAGCTGACATGTTCTTCTCCACTTCGCGGNTCCCTTCCACAGGKCCATG 480
    |||
    |||
    |||
Db 421 GTGTACAGCTGACATGTTCTTCTCCACTTCGCGGNTCCCTTCCACAGGKCCATG 480
QY 481 GTGTCTAATAGATATTTCTATTTCTCAGTGCACGCGGATTTGTCACCTTTGGTTC 540
    |||
    |||
    |||
Db 481 GTGTCTAATAGATATTTCTATTTCTCAGTGCACGCGGATTTGTCACCTTTGGTTC 540
QY 541 CCTGATGTTGGTCTCTTACGCTGGAAGAACTAAACATTTGGTGAATCCAGCCATG 600
    |||
    |||
    |||
Db 541 CCTGATGTTGGTCTCTTACGCTGGAAGAACTAAACATTTGGTGAATCCAGCCATG 600
QY 601 TGACCTTTAAACCTATGAGATGATGATGACAGCTTCGCTCAACAGGAATGATGATG 660
    |||
    |||
    |||
Db 601 TGACCTTTAAACCTATGAGATGATGATGACAGCTTCGCTCAACAGGAATGATGATG 660
QY 661 TCAAGCAATTCATGATTAACCTCTACCTCAATGATGATGACGCTACTA 709
    |||
    |||
    |||
Db 661 TCAAGCAATTCATGATTAACCTCTACCTCAATGATGATGACGCTACTA 709

RESULT 3
US-09-216-386-2
; Sequence 2, Application US/09216386
; Patent No. 6093561

```

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,386
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-216-386-2

Query Match 99.8%; Score 707.6; DB 3; Length 709;
Best Local Similarity 100.0%; Pred. No. 4.3e-226;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGCTCGACAGCCCTTGGGCGCGCGCGCGCGCGCTTCCCTCCGCTGGCGCTGTG 60
DB 1 GCCGCTCGACAGCCCTTGGGCGCGCGCGCGCGCGCTTCCCTCCGCTGGCGCTGTG 60
QY 61 AGCTGAGCGGTGTATGTGCGGCAATACATGTCAACCCCGCTGCCGCTGCGCG 120
DB 61 AGCTGAGCGGTGTATGTGCGGCAATACATGTCAACCCCGCTGCCGCTGCGCG 120
QY 121 CCGCGCGAAGGCGCGCTGCGGTGATTTCTGCATGATGTTGGGATATCGGGCTG 180
DB 121 CCGCGCGAAGGCGCGCTGCGGTGATTTCTGCATGATGTTGGGATATCGGGCTG 180
QY 181 TTAGGCGCTGTACATTAATATGAACGTGCGTATGCTTCATGTTGATTTATGGG 240
DB 181 TTAGGCGCTGTACATTAATATGAACGTGCGTATGCTTCATGTTGATTTATGGG 240
QY 241 TTTCACCGAGATTCACAGAGAGATATCTGGGATTAACAGGACGAGAAATATAAG 300
DB 241 TTTCACCGAGATTCACAGAGAGATATCTGGGATTAACAGGACGAGAAATATAAG 300
QY 301 CTTTGATGATCAGAGAGTGAAGTGAATGSCATTCCTTCAACAGATTAATTTGGAGGT 360
DB 301 CTTTGATGATCAGAGAGTGAAGTGAATGSCATTCCTTCAACAGATTAATTTGGAGGT 360
QY 361 TTCTCAGAGGAGAGCTTTATCTTATATCTGCTTACACACAGACAGAAATGCGAG 420
DB 361 TTCTCAGAGGAGAGCTTTATCTTATATCTGCTTACACACAGACAGAAATGCGAG 420
QY 421 GTGTCACGTGACCTAGTTTCTGTCTTCACCTGGGATTCCTTCCACAGGCKCTATGC 480
DB 421 GTGTCACGTGACCTAGTTTCTGTCTTCACCTGGGATTCCTTCCACAGGCKCTATGC 480

DB 421 GTGTCACGTGACCTAGTTTCTGTCTTCACCTGGGATTCCTTCCACAGGCKCTATGC 480
QY 481 GTGTCCTAATAGATATTTCTATTTCTCCAGTCCACGGGATTTGACCTTTGGTTC 540
DB 481 GTGTCCTAATAGATATTTCTATTTCTCCAGTCCACGGGATTTGACCTTTGGTTC 540
QY 541 CCGTGATGTTGGTTCCTTACGGTGGAAAACTAAACATTTGGTGAATCCAGCCCATG 600
DB 541 CCGTGATGTTGGTTCCTTACGGTGGAAAACTAAACATTTGGTGAATCCAGCCCATG 600
QY 601 TGACCTTTAAACCTATGAGATGATGATGCAAGTTCGTCTCAACAGAAATGATGATG 660
DB 601 TGACCTTTAAACCTATGAGATGATGATGCAAGTTCGTCTCAACAGAAATGATGATG 660
QY 661 TCAAGCAATTCATGATTAACCTCCTACCTCCATTTGATTTAGCTACTA 709
DB 661 TCAAGCAATTCATGATTAACCTCCTACCTCCATTTGATTTAGCTACTA 709

RESULT 4

US-09-213-394-2
Sequence 2, Application US/09213394
Patent No. 6319701

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,394
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0269 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOT19
CLONE: 2676650
US-09-213-394-2

Query Match 99.8%; Score 707.6; DB 4; Length 709;
Best Local Similarity 100.0%; Pred. No. 4.3e-226;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCGCTCGACAGCCCTTGGGCGCGCGCGCGCGCTTCCCTCCGCTGGCGCTGTG 60
DB 1 GCCGCTCGACAGCCCTTGGGCGCGCGCGCGCGCGCTTCCCTCCGCTGGCGCTGTG 60


```

US-09-216-386-4
; Sequence 4, Application US/09216386
; Patent No. 6093561
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,386
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0269-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1486 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-216-386-4

Query Match      88.6%; Score 628.4; DB 3; Length 1486;
Best Local Similarity 91.0%; Pred. No. 1.9e-199;
Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

```

```

355 GAGGGTTTCTCAGAGGAGAGAGCTTTATCTTATATCTGCGCTTACACAGACAGAAAC 414
422 GAGGGTTTCTCAGAGGAGAGAGCTTTATCTTATATCTGCGCTTACACAGACAGAAAC 481
415 TGGCAGGTGTACTGCACCTAGTTCTTGGCTTCCACTGGGGTTCTTCCACAGAGGC 474
482 TGGCAGGTGTACTGCACCTAGTTGGCTTCCACTGGGGTTCTTCCACAGAGGC 541
475 CTATCGGTGTCTTAATAGATATTTCTATCTCCAGTCCACGGGGAGTTGACCTT 534
542 CTATCGGTGTCTTAATAGATATTTCTATCTCCAGTCCACGGGGAGTTGACCTT 601
535 TGGTCCCTGATGTGTGTCTTCTTACGGTGGAAAAAATAAAGATTGGATCCAG 594
602 TGGTCCCTGATGTGTGTCTTCTTACGGTGGAAAAAATAAAGATTGGATCCAG 661
595 CCAATGTGACCTTTAAACCTATGAAGTATGATGACACAGTGTCTCAACAGAAATGA 654
662 CCAATGTGACCTTTAAACCTATGAAGTATGATGACACAGTGTCTCAACAGAAATGA 721
655 TGGATGTCAAGCAATTTATGATTAACCTCTACTCCATTTGATGACCTCACTA 709
722 TGGATGTCAAGCAATTTATGATTAACCTCTACTCCATTTGATGACCTCACTA 776

RESULT 7
US-09-629-645A-18
; Sequence 18, Application US/09629645A
; Patent No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629,645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 18
; LENGTH: 1556
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (195)...(887)
; US-09-629-645A-18

Query Match      88.6%; Score 628.4; DB 4; Length 1556;
Best Local Similarity 91.0%; Pred. No. 1.9e-199;
Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

```

Db 421 TTGGGCTTTCACAGATTCACAGAGGATGATCTGGATTAAACAGGACGAGAAAATA 480
QY 295 TAAAGCTTTGATTCAGAGAGTGAAGATGGCATTCCTCTTAACAGAAATTTTGG 354
Db 481 TAAAGCTTTGATTCAGAGAGTGAAGATGGCATTCCTCTTAACAGAAATTTTGG 540
QY 355 GAGGCTTTTCAGAGGAGGAGCTTTATCTTATATACCTGCTTACACAGACAGAAAC 414
Db 541 GAGGCTTTTCAGAGGAGGAGCTTTATCTTATATACCTGCTTACACAGACAGAAAC 600
QY 415 TGGCAGGTGCATGCACCTAGCTTCTGCTCCACTGCGGNTCCCTTTCACAGAGGC 474
Db 601 TGGCAGGTGCATGCACCTAGCTTCTGCTCCACTGCGGNTCCCTTTCACAGAGGC 660
QY 475 CTATCGGTGGCTAAAGAGATATTTCTATCTCCAGTCCAGCGGAGATGGACCCCT 534
Db 661 CTATCGGTGGCTAAAGAGATATTTCTATCTCCAGTCCAGCGGAGATGGACCCCT 720
QY 535 TGGTCCCTGATGTTTGGTCTCTTACGGTGGAAAACTTAAACATTTGGTGAATCCAG 594
Db 721 TGGTCCCTGATGTTTGGTCTCTTACGGTGGAAAACTTAAACATTTGGTGAATCCAG 780
QY 595 CCAATGTGACCTTTAAACCTATGAGAGTATGATGCACAGTGTGCTCAACAGAAATGA 654
Db 781 CCAATGTGACCTTTAAACCTATGAGAGTATGATGCACAGTGTGCTCAACAGAAATGA 840
QY 655 TGGATGCAAGCAATTCATGATTAACCTCTACTCCCAATTTGATGACGCTACTA 709
Db 841 TGGATGCAAGCAATTCATGATTAACCTCTACTCCCAATTTGATGACGCTACTA 895

RESULT 8

US-09-629-645A-3
; Sequence 3, Application US/09629645A
; Patient No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629,645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 3
; LENGTH: 2417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(728)
US-09-629-645A-3

Query Match

Best Local Similarity 83.1%; Score 589.4; DB 4; Length 2417;
Best Local Similarity 90.5%; Pred. No. 2.7e-186;
Matches 666; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

QY 40 CTTCCTTCGCGCTGCGGTGAGCTGAGCGGTGTATGTGCGGCATTAACATGCAACCC 99
Db 1 CTTCCTTCGCGCTGCGGTGAGCTGAGCGGTGTATGTGCGGCATTAACATGCAACCC 60
QY 100 CGCTGCCCGGCATGTCGCCGCCGCCGGAAGGCCACCGCTGGCGATTTTCTGCATG 159
Db 61 CGCTGCCCGGCATGTCGCCGCCGCCGGAAGGCCACCGCTGGCGATTTTCTGCATG 120
QY 160 GATTGGAGTACTG----- 175
Db 121 GATTGGAGTACTGCGACAGATGGGAGAACCTTTCAGAGTATCAGAAATTCACATA 180
QY 176 -----GCCTGTTAGGCGCTGTACATTAATTAATGAGCGTGGCA 213
Db 181 TCATAATATATCTCCCGCATGCCCTGTATAGGCTGTACATTAATTAATGAGCGTGGCA 240
QY 214 TGCCTTCATGTTGATATATATGAGCTTTCACAGATTCACAGAGATGATGATCGGA 273

Db 241 TGCCTTCATGTTGATATATATGAGCTTTCACAGATTCACAGAGATGATGATCGGA 300
QY 274 TTAACAGGACAGAGAAATATTAAGCTTTGATGATCAAGAGTGAAGATGGCATTC 333
Db 301 TTAACAGGACAGAGAAATATTAAGCTTTGATGATCAAGAGTGAAGATGGCATTC 360
QY 334 CTTCATACAGAAATATTTGGAGGTTTCTCAGGAGGAGCTTATCTTATATAGTG 393
Db 361 CTTCATACAGAAATATTTGGAGGTTTCTCAGGAGGAGCTTATCTTATATAGTG 420
QY 394 CCTTACACAGAGAGAAATGCGAGGTGTCATGCACTAGTATGTTCTGCTCCACTTC 453
Db 421 CCTTACACAGAGAGAAATGCGAGGTGTCATGCACTAGTATGCTGGCTCCACTTC 480
QY 454 GGGATTCCTTTCACAGAGGKCTATGCGGTGCTGCTAATAGAGATATTTCTATCTCCAGT 513
Db 481 GGGCTTCCTTTCACAGAGGKCTATGCGGTGCTGCTAATAGAGATATTTCTATCTCCAGT 540
QY 514 GCGAGGGGATGTGACCCCTTGTCCCTGATGTTGGTGTCTTACGGTGGAAAAAC 573
Db 541 GCGAGGGGATGTGACCCCTTGTCCCTGATGTTGGTGTCTTACGGTGGAAAAAC 600
QY 574 TAAACATTTGGTGAATCCAGCCATGTGACCTTAAACCTATGAGATGATGACACA 633
Db 601 TAAACATTTGGTGAATCCAGCCATGTGACCTTAAACCTATGAGATGATGACACA 660
QY 634 GTTCGTGTCACAGAGAAATGATGATGTCACAGCAATTTATGATTAACCTCTACTCCAA 693
Db 661 GTTCGTGTCACAGAGAAATGATGATGTCACAGCAATTTATGATTAACCTCTACTCCAA 720
QY 694 TTGATTGACGCTACTA 709
Db 721 TTGATTGACGCTACTA 736

RESULT 9

US-09-629-645A-10
; Sequence 10, Application US/09629645A
; Patient No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629,645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 10
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(693)
US-09-629-645A-10

Query Match

Best Local Similarity 61.5%; Score 436; DB 4; Length 693;
Best Local Similarity 79.9%; Pred. No. 1.8e-135;
Matches 554; Conservative 1; Mismatches 72; Indels 66; Gaps 1;

QY 75 ATGTGCGCAATTAACATGCAACCGCTGCGGCATGTCGCCGCCGGAAGAGCC 134
Db 1 ATGTGCGCAATTAACATGTCGCTCCGATGCCGCCGCTTGTGCGGCCGCCGGAAGAGCC 60
QY 135 ACCGCTGGCGATTTTCTCAGATGATGGAGATAGCTGG----- 176
Db 61 ACCGCGCGGATATTTCTCAGAGATGGAGATACAGGAGATGATGGAGAGAGCC 120
QY 177 -----CTGTTAGGCTT 188
Db 121 TTTGAGGATACAAAGTCCCGACATCAAAATACATCTGTCCACATGCCCCCTGTGATGCCA 180

Qy	189	GTTCATTAAATATGAACTGGCTATAGCCCTCACTGGTTTGATTAATATGGGCTTTACCA	248
Db	181	GTTCATTAAATATGAAATATGCTATAGCCCTCTTGGTTTGATTAATCGTTGACCTTTCACCA	240
Qy	249	GATTCACAGAGAGATGTAATCTGGGATTTAAACAGGACAGCAAAATATAAAGCTTTGATTT	308
Db	241	GATTCACAGAGAGATGTAATCTGGGATTTAAACAGGACAGCAAAATATAAAGCTTTGATTT	300
Qy	309	GATCAAGAAGTGAAGATGGCATTTCTCTTCAACAGATTAATTTTGGAGGCTTTTCTCAG	368
Db	301	GATCAAGAAGTGAAGATGGCATTTCTCTTCAACAGATTAATTTTGGAGGATTTTCTCAG	360
Qy	369	GGAGAGCTTTATTTATATATACCTGGCCCTTACACACAGACAGCAAACTGGACGGTGTACT	428
Db	361	GGAGAGCTTTATTTATATATACCTGGCCCTTACACACAGACAGCAAACTGGTGTGTACT	420
Qy	429	GCACCTAGTTCTTGGCTTCCACTTCCTGGGATTTCCCTCTTCCACAGGACCTATGCGTGCT	488
Db	421	GCACCTAGTTCTTGGCTTCCACTTCCTGGGATTTCCCTCTTCCACAGGACCTATGCGTGCT	480
Qy	489	AATGAGATATTTCTATTTCTCCAGTGGCCACAGGGGATTTGACCCCTTTGTTCCCTGATG	548
Db	481	AATGAGATATTTCTATTTCTCCAGTGGCCACAGGGGATTTGACCCCTTTGTTGCTGATG	540
Qy	549	TTTGTTCTCTTACGGGTGGAAACATTAACATTTGGTGAATCCAGCAATGTGACCTTT	608
Db	541	TTTGTTCTCTTACGGGTGGAAACATTAACATTTGGTGAATCCAGCAATGTGACCTTT	600
Qy	609	AAAACCTATGAAGGTATGATGACAGACTTGGTGTCAACAGAGAAATGATGATGTCAACAA	668
Db	601	AAAATCTATGAAGGTATGATGACAGACTTGGTGTCAACAGAGAAATGATGATGTCAACAC	660
Qy	669	TTTCATGTATAACCTCACTCCATTAATGTATGA	701
Db	661	TTTCATGTATAAGCTCCTCACTCCATTAATGTATGA	693
RESULT 10			
US-09-629-645A-21			
; Sequence 21, Application US/09629645A			
; Patent No. 6365354			
; GENERAL INFORMATION:			
; APPLICANT: C. Frank Bennett			
; APPLICANT: Jacqueline Wyatt			
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYOPHOSPHOLIPASE I EXPRESSION			
; FILE REFERENCE: RTS-0137			
; CURRENT APPLICATION NUMBER: US/09/629,645A			
; NUMBER OF SEQ ID NOS: 164			
; SEQ ID NO 21			
; LENGTH: 727			
; TYPE: DNA			
; ORGANISM: Mus musculus			
; FEATURE:			
; NAME/KEY: unsure			
; LOCATION: 639			
; OTHER INFORMATION: unknown			
; NAME/KEY: unsure			
; LOCATION: 684			
; OTHER INFORMATION: unknown			
; NAME/KEY: unsure			
; LOCATION: 712			
; OTHER INFORMATION: unknown			
; NAME/KEY: unsure			
; LOCATION: 719			
; OTHER INFORMATION: unknown			
; NAME/KEY: CDS			
; LOCATION: (36)...(727)			
; US-09-629-645A-21			

Query Match	61.1%;	Score 433.2;	DB 4;	Length 727;
Best Local Similarity	79.1%;	Pred. No. 1.6e-134;		
Matches 553;	Conservative 1;	Mismatches 79;	Indels 66;	Gaps 1;

QY	66	AGGGCGGTATGTGGGGCAATTAACATGTCACACCCGGCGCCGGCATGCGCCGGCC	125
Db	29	AGCGGTGGATGTGGGGCAACACATGTGCGCTCCGATGCCCGCGCTGTGCCGGCCGC	88
QY	126	CGGAAGGCCACCGCTGGCGGTATTTTCTGCATGGATTTGGAGACTGGG-----	176
Db	89	CGGAAGGGCCACCGCGCGGTATTTTCTTCACGGATTTGGAGATACAGGGCATGATGG	148
QY	177	-----CCT	179
Db	149	GCAGAAGCCTTTGCAGGTATATAAAGTCCCATCAAATTCATCTGTCCATGCCCT	208
QY	180	GTTAGGCGCTGTATTAATTAATGAACGTGGCTATGCGCTCATGGTTGATATTATGGG	239
Db	209	GTGATGCCAGTCACATTAATATGAAATATGCTATGCGCTTCTTGTTGATTCGTTGGA	268
QY	240	CTTTACCACGATTCACAGSAGATGAATCTGGGATTTAAACAGCAGCAGAAATATATAA	299
Db	269	CTTTACCACGATTCACAGSAGATGAATCTGGGATTTAAACAGCAGCAGAAACCGTAAAA	328
QY	300	GCTTTGATTGATCAAGAAGTGAAGATGGCATTCCTCTTAACACAGATTTATTTTGGAGGG	359
Db	329	GCGTTGATGAATCAAGAAGTGAAGATGGCATTCCTCTTAACAGGATTTATTTTGGAGGA	388
QY	360	TTTTCTCAGGAGAGCTTTATCTTTATATACGCCCTTACACACAGCAGAAACTGGCA	419
Db	389	TTTTCTCAGGAGAGCGGCTTGTCTTTATACCTGCTCTCACACACAGCAGAAACTGGCT	448
QY	420	GGTGCACATGCACTCAGTTTCTTCTTCACATTTGGGNTTCCTTCCACAGGGACCTATC	479
Db	449	GGTGCACATGCACTCAGTTTCTTCTTCACATTTGGGNTTCCTTCCACAGGGACCTATC	508
QY	480	GGTGTGCTAATAGAGATATTTTATTTCTCCAGTGGCCACGGGGAATTTGACCTTTGGTT	539
Db	509	AACATGTCTATCCAGATATTTTCGTTCTCCAGTGGCCATGAGATTTGACCTTAGTT	568
QY	540	CCCCGATGTTGGTCTCTTAGGTTGGAAAACTATAAACATTTGGATTCACAGCAAT	599
Db	569	CCCCTAATGTTGGTCTCTTAGTGTGAAGACTATAACCATTTGATTAATTCACAGCAAT	628
QY	600	GTGACCTTTAAACCTATGAAGGTATGATGACAGTTCGTGTCAACAGSAAATGATGAT	659
Db	629	GTACCTTCANAAATCTATGAAGGATGATGACAGTTCATGTCCAGCAGSAAATGATGAT	688
QY	660	GTCAAGCATTCATGATTAACCTCTCACTCCCAATTGAT	698
Db	689	GTCAAGCATTCATGATTAAGCTCTCACTCCCAATTGAT	727

```

1 RESULT 11
2 US-09-013-881-15
3 : Sequence 15, Application US/09013881
4 : Patent No. 6132964
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: Bandman, Olga
9 :
10 : APPLICANT: Lal, Preeli
11 :
12 : APPLICANT: Hillman, Jennifer L.
13 :
14 : APPLICANT: Corley, Neil C.
15 :
16 : APPLICANT: Guegler, Karl J.
17 :
18 : APPLICANT: Shah, Purvi
19 :
20 : TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
21 :
22 : NUMBER OF SEQUENCES: 16
23 :
24 : CORRESPONDENCE ADDRESS:
25 :
26 : ADDRESSEE: Incyte Pharmaceuticals, Inc.
27 :
28 : STREET: 3174 Porter Drive
29 :
30 : CITY: Palo Alto
31 :
32 : STATE: CA
33 :
34 : COUNTRY: USA
35 :
36 : ZIP: 94304
37 :
38 : COMPUTER READABLE FORM:
39 :
40 : MEDIUM TYPE: Diskette
41 :
42 : COMPUTER: IBM Compatible

```

Query Match 30.6%;	Score 217.2;	DB 3;	Length 1624;
Best Local Similarity 64.9%;	Pred. No. 3.4e-62;		
Matches 337; Conservative	0; Mismatches 179;	Indels 3;	Gaps 1

RESULT 12
US-09-629-645A-20
; Sequence 20, Application US/09629645A
; Patent No. 6365354

Query Match	12.88;	Score 90.6;	DB 4;	Length 608;
Best Local Similarity	91.4%;	Pred. No. 3.1e-20;		
Matches	96;	Conservative	9;	Indels 0;
		Mismatches	9;	Gaps 0

RESULT 13
US-09-216-001-2
; Sequence 2, Application US/09216001

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

100

Tue Jan 21 10:18:37 2003

us-09-988-982-2.rni

Page 10

Db 966 TGACGCACTAGAAAAGATCCTATCCCTGAAACATTTACTGTTTATAGA 1014

Search completed: January 19, 2003, 03:15:21
Job time : 80 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2003, 01:38:35 ; Search time 100 Seconds
(without alignments)
3161.206 Million cell updates/sec

Title: US-09-988-982-2

Perfect score: 709

Sequence: 1 GCCCGTCGACGCCCTTGGG.....CCAATTGATTGACGTCACTA 709

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 393868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	707.6	99.8	709	US-09-988-982-2	Sequence 2, Appl1
2	628.4	88.6	2493	US-09-925-299-218	Sequence 218, App
3	589.4	83.1	2417	US-09-813-358-221	Sequence 221, App
4	392.4	55.3	416	US-10-046-935-1369	Sequence 1369, Ap
5	392.4	55.3	416	US-09-878-178-1369	Sequence 1369, Ap
6	230.2	31.1	441	US-09-960-352-3924	Sequence 3924, Ap
7	126	17.8	782	US-09-813-358-220	Sequence 220, App
8	119.8	16.9	461	US-09-813-358-207	Sequence 207, App
9	99.4	14.0	106	US-09-998-598-2083	Sequence 2083, Ap
10	79.2	11.2	105	US-09-796-692-5977	Sequence 5977, Ap
11	55.8	7.9	589	US-09-969-347-51	Sequence 51, Appl
12	55.8	7.9	802	US-09-833-381-1895	Sequence 1895, Ap
13	51.8	7.3	583	US-09-833-381-1894	Sequence 1894, Ap
14	36	5.1	396	US-09-853-386-88	Sequence 88, Appl
15	35.6	5.0	6659	US-09-321-987B-1	Sequence 1, Appl1
16	35.2	5.0	561	US-09-833-381-1893	Sequence 1893, Ap
17	35	4.9	116592	US-09-818-512-3	Sequence 3, Appl1
18	34.4	4.9	9824	US-09-853-386-13	Sequence 13, Appl1
19	34.4	4.9	10883	US-09-853-386-13	Sequence 13, Appl1

20 33.8 4.8 1356 10 US-09-967-805-8 Sequence 8, Appl1

21 33.6 4.7 88421 9 US-09-976-059-1 Sequence 1, Appl1

22 32.2 4.5 376 10 US-09-983-965-4282 Sequence 4282, Ap

23 32.2 4.5 29344 10 US-09-464-767-1 Sequence 1, Appl1

24 32.2 4.5 32745 10 US-09-464-767-3 Sequence 3, Appl1

25 32 4.5 945 10 US-09-886-055-360 Sequence 360, App

26 32 4.5 4800 9 US-09-738-626-810 Sequence 810, App

27 31.8 4.5 2000 9 US-09-938-842-3144 Sequence 3144, Ap

28 31.6 4.5 727 10 US-09-910-943-478 Sequence 478, App

29 31.4 4.4 4257 9 US-09-825-2884-1 Sequence 1, Appl1

30 31.2 4.4 289 10 US-09-294-093B-992 Sequence 992, App

31 31.2 4.4 197997 10 US-09-822-246-3 Sequence 3, Appl1

32 31.2 4.4 640681 10 US-09-790-988-1 Sequence 1, Appl1

33 31 4.4 386 10 US-09-783-590-11377 Sequence 11377, A

34 31 4.4 465 10 US-09-864-761-16083 Sequence 16083, A

35 31 4.4 686 9 US-09-930-125-13 Sequence 13, Appl1

36 30.8 4.3 460 10 US-09-791-171-89 Sequence 89, Appl1

37 30.8 4.3 1104 9 US-09-894-844-3 Sequence 91, Appl1

38 30.8 4.3 1200 10 US-09-791-171-91 Sequence 91, Appl1

39 30.8 4.3 1500 10 US-09-922-501-11 Sequence 11, Appl1

40 30.8 4.3 1617 10 US-09-023-588-67 Sequence 67, Appl1

41 30.8 4.3 2606 10 US-09-837-654-7 Sequence 7, Appl1

42 30.8 4.3 2606 10 US-09-837-654-7 Sequence 7, Appl1

43 30.8 4.3 2754 10 US-09-861-801-3 Sequence 3, Appl1

44 30.8 4.3 3439 10 US-09-837-654-6 Sequence 6, Appl1

45 30.8 4.3 3439 10 US-09-837-654-6 Sequence 6, Appl1

ALIGNMENTS

RESULT 1

US-09-988-982-2

; Sequence 2, Application US/09988982

; Patent No. US20020081699A1

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

Murry, Lynn E.

NUMBER OF SEQUENCES: 3

TITLE OF INVENTION: NOVEL HUMAN LYXOPHOSPHOLIPASE

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,982

FILING DATE: 19-NO. US20020081699A1-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/213,394

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0269 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 709 base pairs

TYPE: nucleic acid

STRANDEDNESS: Single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: KIDN00119
CLONE: 2676650
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-988-982-2

Query Match 99.8%; Score 707.6; DB 10; Length 709;
Best Local Similarity 100.0%; Pred. No. 2,9e-211;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GCGCTGCGACGCGCTTGGCGCGCGCGCGCGCGCTTCCCTTCCGTTGGCGCTGTG 60
    |||||||
DB 1 GCGCTGCGACGCGCTTGGCGCGCGCGCGCGCGCGCTTCCCTTCCGTTGGCGCTGTG 60
QY 61 ACCTGAGCGCGGTGATGTGCGGCAATTAACATGTCAACCCCGCGCCCATCTGCGCCG 120
    |||||||
DB 61 ACCTGAGCGCGGTGATGTGCGGCAATTAACATGTCAACCCCGCGCCCATCTGCGCCG 120
QY 121 CCGCGCGGAAAGCCACCGCTGGGCGGTGATTTCCCATGAGATGGAGATCTGGGCGCTG 180
    |||||||
DB 121 CCGCGCGGAAAGCCACCGCTGGGCGGTGATTTCCCATGAGATGGAGATCTGGGCGCTG 180
QY 181 TTAGCGCTGTACATTAATATGAACGTGCGTATGCTCTCATGCTTGTGATATTTGGGC 240
    |||||||
DB 181 TTAGCGCTGTACATTAATATGAACGTGCGTATGCTCTCATGCTTGTGATATTTGGGC 240
QY 241 TTTTCACAGATTACAGAGAGATGATCTGGATTAACAGCAGCAGCAAAATATTAAG 300
    |||||||
DB 241 TTTTCACAGATTACAGAGAGATGATCTGGATTAACAGCAGCAGCAAAATATTAAG 300
QY 301 CTTTGATGATCAGAGAGATGAGATGAGATGATCTCTTCAACAGATTAATTTGGGAGGT 360
    |||||||
DB 301 CTTTGATGATCAGAGAGATGAGATGAGATGATCTCTTCAACAGATTAATTTGGGAGGT 360
QY 361 TTTTCTCAGGAGAGCTTTATCTTTATATATCTGCTTACACACAGCAGCAACTGGCAG 420
    |||||||
DB 361 TTTTCTCAGGAGAGCTTTATCTTTATATATCTGCTTACACACAGCAGCAACTGGCAG 420
QY 421 GGTGCTCAGCAGCTGCTTCTGCTTCCACTTCCGCGGNTCCCTTCCACAGGCGCTATCG 480
    |||||||
DB 421 GGTGCTCAGCAGCTGCTTCTGCTTCCACTTCCGCGGNTCCCTTCCACAGGCGCTATCG 480
QY 481 GTGTGCTATAGATATTTCTATCTTCTCAGTGCACGCGGAGTTGTGACCTTTGGTTC 540
    |||||||
DB 481 GTGTGCTATAGATATTTCTATCTTCTCAGTGCACGCGGAGTTGTGACCTTTGGTTC 540
QY 541 CCTGTATGTTGTTCTCTTACGGTGGAAAACTAAACATTTGGGATTCAGCCATG 600
    |||||||
DB 541 CCTGTATGTTGTTCTCTTACGGTGGAAAACTAAACATTTGGGATTCAGCCATG 600
QY 601 TGACCTTTAAACCTATGAGGATGATGACAGATTCGTCTCAACAGCAAAATGATGATG 660
    |||||||
DB 601 TGACCTTTAAACCTATGAGGATGATGACAGATTCGTCTCAACAGCAAAATGATGATG 660
QY 661 TCAAGCAATTCATGATTAACCTCTACCTCCATTCATGATTGAGCTACTA 709
    |||||||
DB 661 TCAAGCAATTCATGATTAACCTCTACCTCCATTCATGATTGAGCTACTA 709
```

RESULT 2

US-09-925-299-218
Sequence 218, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 218
LENGTH: 2493
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-299-218

Query Match 88.6%; Score 628.4; DB 10; Length 2493;
Best Local Similarity 91.0%; Pred. No. 3.6e-186;
Matches 705; Conservative 1; Mismatches 3; Indels 66; Gaps 1;

```
QY 1 GCGCTGCGACGCGCTTGGCGCGCGCGCGCGCGCTTCCCTTCCGTTGGCGCTGTG 60
    |||||||
DB 26 GCGCTGCGACGCGCTTGGCGCGCGCGCGCGCGCGCTTCCCTTCCGTTGGCGCTGTG 85
QY 61 ACCTGAGCGCGGTGATGTGCGGCAATTAACATGTCAACCCCGCGCCCATCTGCGCCG 120
    |||||||
DB 86 ACCTGAGCGCGGTGATGTGCGGCAATTAACATGTCAACCCCGCGCCCATCTGCGCCG 145
QY 121 CCGCGCGGAAAGCCACCGCTGGGCGGTGATTTCCCATGAGATGGAGATCTGGGCGCTG 175
    |||||||
DB 146 CCGCGCGGAAAGCCACCGCTGGGCGGTGATTTCCCATGAGATGGAGATCTGGGCGCTG 205
QY 176 ----- 175
DB 206 GATGGCGAGAGCTTTGACGATATCAGAAATTCACATATCAATATATCTGCCCATG 265
QY 176 -GCTGTGAGCGCTTACATTAATATGAACGTGCTATGCTTCACTGTTGATATTA 234
    |||||||
DB 266 GCGCTGTGAGCGCTTACATTAATATGAACGTGCTATGCTTCACTGTTGATATTA 325
QY 235 TTTGGCTTTTACAGATTCACAGAGAGATGAATCTGGGATTAACAGCAGCAGAAAAATA 294
    |||||||
DB 326 TTTGGCTTTTACAGATTCACAGAGAGATGAATCTGGGATTAACAGCAGCAGAAAAATA 385
QY 295 TAAAGCTTTGATGATCAGAAATGAAGATGAGATTTCTTCAACAGAAATATTTGG 354
    |||||||
DB 386 TAAAGCTTTGATGATCAGAAATGAAGATGAGATTTCTTCAACAGAAATATTTGG 445
QY 355 GAGGCTTTTTCAGAGGAGAGCTTTATCTTATATCTGCTTACACAGCAGCAGAAAC 414
    |||||||
DB 446 GAGGCTTTTTCAGAGGAGAGCTTTATCTTATATCTGCTTACACAGCAGCAGAAAC 505
QY 415 TGGCAGGTGTCAGTCACTAGTTCTTCTGCTTCCACTTCCGAGNTTCTTTCACAGGK 474
    |||||||
DB 506 TGGCAGGTGTCAGTCACTAGTTCTGCTTCCACTTCCGAGNTTCTTTCACAGGK 565
QY 475 CTATCGGTGGGCTAAATGAGATATTTCTATCTCCAGTGCACGCGGAGTTGTACCTT 534
    |||||||
DB 566 CTATCGGTGGGCTAAATGAGATATTTCTATCTCCAGTGCACGCGGAGTTGTACCTT 625
QY 535 TGGTCCCTGATGTTGGTCTCTTACGGTGGAAAACTAAACATTTGGTGAATCCAG 594
    |||||||
DB 626 TGGTCCCTGATGTTGGTCTCTTACGGTGGAAAACTAAACATTTGGTGAATCCAG 685
QY 595 CCAATGTACCTTTAAACCTATGAGGATGATGACAGATTCGTCTCAACAGCAAAATGA 654
    |||||||
DB 686 CCAATGTACCTTTAAACCTATGAGGATGATGACAGATTCGTCTCAACAGCAAAATGA 745
QY 655 TGGATGTCAGCAATTCATGATTAACCTCTACCTCCATTCATGATTGAGCTACTA 709
    |||||||
DB 746 TGGATGTCAGCAATTCATGATTAACCTCTACCTCCATTCATGATTGAGCTACTA 800
```

RESULT 3

US-09-813-358-221
Sequence 221, Application US/09813358
Patent No. US20020048759A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Pyle, Ruth
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

Query Match	55.38;	Score 392.4;	DB 9;	Length 416;
Best Local Similarity	99.08;	Pred. No. 7.4e-113;		
Matches 393;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;

QY	313	AAGAGTAAAGATGGCATTCCTCTTAACAGATAATATTTTGGAGGGTTTCTCAGGAG	372
Db	416	AAGAGTAAAGATGGCATTCCTCTTAACAGATAATATTTTGGAGGGTTTCTCAGGAG	357
QY	373	GAGCTTATCTTATATACTGCCCTTACACAGCAGAGAAACTGGCAGGTCTCACTGCAC	432
Db	356	GAGCTTATCTTATATACTGCCCTTACACAGCAGAGAAACTGGCAGGTCTCACTGCAC	297
QY	433	TCAGTTTCTTCTTCACATTGGGGTTCCTTCCACAGGGACCTATCGGTGTGCTAATA	492
Db	296	TCAGTTTCTTCTTCACATTGGGGTTCCTTCCACAGGGACCTATCGGTGTGCTAATA	237
QY	493	GAGATATTTCTAATTCCTCAGTGCACAGGGAGATGTGACCCCTTGGTTCCTCGATGTTTG	552
Db	236	GAGATATTTCTAATTCCTCAGTGCACAGGGAGATGTGACCCCTTGGTTCCTCGATGTTTG	177
QY	553	GTTCTCTTACGGTGGAAAACTTAAACATTTGGTGAATCCAGCCAAATGTGACTTTTAAA	612
Db	176	GTTCTCTTACGGTGGAAAACTTAAACATTTGGTGAATCCAGCCAAATGTGACTTTTAAA	117
QY	613	CCATATGAAGGTATGATGCACAGTTCTGTCTCAACAGGAATATGATGTCTCAAGCAATTCA	672
Db	116	CCATATGAAGGTATGATGCACAGTTCTGTCTCAACAGGAATATGATGTCTCAAGCAATTCA	57
QY	673	TTGATAAACCTCACTCCCTCAATGTGATGAGTCACTA 709	
Db	56	TTGATAAACCTCACTCCCTCAATGTGATGAGTCACTA 20	

```

RESULT 6
US-09-960-352-3924
: Sequence 3924, Application US/09960352
: Patent No. US20020137139A1
:
GENERAL INFORMATION:
: APPLICANT: Warren, Wesley C.
: APPLICANT: Tao, Nengbing
: APPLICANT: Byatt, John C.
: APPLICANT: Mathialagan, Nagappan
: TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
: TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
: FILE REFERENCE: 16511.006/37-21(10298)C
: CURRENT APPLICATION NUMBER: US/09/960.352
: CURRENT FILING DATE: 2001-09-24
: NUMBER OF SEQ ID NOS: 15112
: SEQ ID NO 3924
: LENGTH: 441
: TYPE: DNA
:
ORGANISM: Bos taurus
:
OTHER INFORMATION: Clone ID: 17-LIB34-018-Q1-E1-E1
US-09-960-352-3924

```

Query Match	31.1%;	Score 220.2;	DB 10;	Length 441;
Best Local Similarity	-76.1%;	Pred. No. 5.3e-59;		
Matches 316; Conservative	0;	Mismatches 33;	Indels 66;	Gaps 1;

OY	69	CGGTTATGTCGGCAATTAACATGTCACACCCGGTGGCCGGCATTCGACCGCCGGC	128
Db	25	CGGTGTATGTCGGCAATTAACATGTCGGCTCCGCTGCCCGCATCTGTCCCTGCCGCCGT	84
OY	129	AAGCCACCGCTGCGCGTATTTCTCTGCATGGATTGGAGATCTAGCGCCT-----	179
Db	85	AAGCCACCGCGCGGTGATCTCTTCATGAGATTGGGACACACGAGCATGATGGGCA	144
OY	180	-----GTT	182
Db	145	GAAGCCTTTGCCGGATTCAGAAAGCGCCCATCATCAATATCATCTGCCCGCATGGCCGTT	204
OY	183	AGGCTGTATCATTTAAATATATGACGTGGCTATGCGCTTCATGTTTGATATTATGGGCTT	242

Db	205	ATGCTGTAACTTTAAATATGAAATGGCCATCATGGTTTGACATTATTGGGCTT	264
Oy	243	TCACCAATTCACAGGAGATGATCTGGATTTAAACAGCGACGAGAAATATTAAGCT	302
Db	265	TGCGCAGATTCACGTGAGAGTGAACCTGGAATTTAAACAGCGACGAGAAATGTTAAAGCT	324
Oy	303	TTCATTGATCAAGAGTGAATAATGCGATTCCTTAAACAGAAATATTGGGAGGGTTT	362
Db	325	TTCATGATCAAGAGTGAATAAGCGGATTCCTTAAACAGAAATATTGGGAGGATTT	384
Oy	363	TTCACAGGAGAGCTTTTCTTTATATACCTGCGCTTACCACACACAGAAACTGG	417
Db	385	TCTCAGGAGAGCTTTTATCTCTGTACACGCGCTTCACACACACAGAAACTGG	439

```

RESULT 7
US-09-813-358-220
; Sequence 220, Application US/09813358
; Patent No. US20020048759A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Pyle, Ruth
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF OVARIAN AND ENDOMETRIAL CANCER
; FILE REFERENCE: 210121.501
; CURRENT APPLICATION NUMBER: US/09/813,358
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 220
; LENGTH: 782
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-813-358-220

```

Query Match	17.8%	Score 126;	DB 10;	Length 782;
Best Local Similarity	100.0%	Pred. No. 2.2e-29;		
Matches 126;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	584	GGGGAATCCAGCAATGTGACCTTTAAACCTATGAAGTATGATGACACAGTGTGTCA	64.3
Db	1	GGGAATCCAGCAATGTGACCTTTAAACCTATGAAGTATGATGACACAGTGTGTCA	60
QY	644	ACAGGAATGATGATGTCAAGCAATCATTTGATTAACCTCTACCTCCAAATTTGATTGACG	70.3
Db	61	ACAGGAATGATGATGTCAAGCAATCATTTGATTAACCTCTACCTCCAAATTTGATTGACG	120
QY	704	TCACCTA 709	
Db	121	TCACCTA 126	

```

1 RESULT 8
2 US-09-813-358-207
3 ; Sequence 207, Application US/09813358
4 ; Patent No. US20020048759A1
5 ;
6 ; GENERAL INFORMATION:
7 ;
8 ; APPLICANT: Xu, Jiaqichun
9 ; APPLICANT: Pyle, Ruth
10 ; APPLICANT: Stolk, John A.
11 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
12 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL
13 ; FILE REFERENCE: 210121.501
14 ; CURRENT APPLICATION NUMBER: US/09/813,358
15 ; CURRENT FILING DATE: 2001-03-21
16 ; NUMBER OF SEQ ID NOS: 222
17 ; SOFTWARE: FastSeq for Windows Version 4.0
18 ;
19 ; SEQ ID NO 207
20 ;
21 ; LENGTH: 461
22 ;
23 ; TYPE: DNA
24 ;
25 ; ORGANISM: Homo sapiens
26 ;
27 ; FEATURE:

```

Query Match	7.9%;	Score 55.8;	DB 10;	Length 589;
Best Local Similarity	51.2%;	Pred. No. 1.6e-07;		
Matches 126;	Conservative 1;	Mismatches 119;	Indels 0;	Gaps 0;

QY	295	TTAAAGCTTATATGATCAACAATAATGAAGATGSCATTCTCTTACAGAAATTATTTGG	354
	1		
	2		
	3		
	4		
	5		
Db	525	TTACTGATTATGATGAGAAAGATTAATAATGGCATCAGAGACACAGGATATTAAATAG	466
	1		
	2		
	3		
	4		
	5		
QY	355	GAGGGTTTTCTCAGGAGAGACCTTATCTTTATATATCTGCCCTTACACACAGCAGAAC	414
	1		
	2		
	3		
	4		
	5		
Db	465	GAGGATTTCTATGGGAGGATGATGCGCAATGCAATTAAGCATATAGAAATCATCATACATG	406
	1		
	2		
	3		
	4		
	5		
QY	415	TGGCAGGTGTACGACACTCAGTTCTTGCTTCCACTTCCGGGNTTCTTTCCACAGGKC	474
	1		
	2		
	3		
	4		
	5		
Db	405	TGGCAGGAGTATTTGGCTCTTTCTAGTTTTCCTGAATTAAGCATCTGCTGTTTACCAAGCTC	346
	1		
	2		
	3		
	4		
	5		
QY	475	CTATGGGTGTCTAATAGAGATATTTCTATTTCTCCAGTGCACAGGGGATTTGACCCCTT	534
	1		
	2		
	3		
	4		
	5		
Db	345	TTCAAGAGATTAATGGTGTACTTCTCTGATTAATTTTCACGTGCATGATGACTGCACAGATAGT	286
	1		
	2		
	3		
	4		
	5		
QY	535	TGGTTC	540
	1		
	2		
	3		
	4		
	5		
Db	285	TAGTTC	280

```

RESULT 12
US-09-833-381-1895/c
; Sequence 1895, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1 Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1895
; LENGTH: 802
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1895

```

Query Match	7.9%	Score 55.8	DB 10	Length 802
Best Local Similarity	51.2%	Pred. No. 1.9e-07		
Matches 126	Conservative 1	Mismatches 119	Indels 0	Gaps 0
QY 295	FAAAGCTTGATGATCAAGAAGCAAAATGGCATTCCTCTTAACACAAATTAATTTGG			354
DB 525	TTACTGATTTGATGTGAAGAAAGTAAAGTGGCATTCAGAAAGACAGATTAATATAG			466
QY 355	GAGGTTTTCTAGGAGGAGGCTTTATCTTATATCTCCCTTACCACACAGACAAGAC			414
DB 465	GAGGATTTCTATGAGGAGATGCATGCGCATTCATTTACCATATAGAAATCATCAAGATG			406
QY 415	TGGCAGGTGTCACTGCATCACTCACTTCTGCTTCACCTTCGGGTTTCCTTTCCACAGGKAC			474
DB 405	TGGCAGAGATTAATTTGCTCTTCTAGTTTCTGAATTAAGCATCTGCTGTTTACCAAGCTC			346
QY 475	CTATCGGTGTGCTAATTAAGATATTTCTATTTCTCCAGTCCACGGGATTTGGACCTT			534
DB 345	TTTCAGAGAGTAAATGGTCTACTCTCCGAATTAATTTTCAGTGTATGTCTACTGACAGATGAGT			286
QY 535	TGGTTC 540			
DB 285	TAGTTC 280			

```

RESULT 13
US-09-833-381-1894
; Sequence 1894, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs

```

```

; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1894
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-833-381-1894

Query Match          7.3%; Score 51.8; DB 10; Length 583;
Best Local Similarity 58.9%; Pred. No. 2.9e-06;
Matches      89; Conservative      0; Mismatches 62; Indels      0; Gaps      0.

```

OY	235	TAAAGCTTTGATGATCAAAAGATGAAGATGCCATTCCTCTCAACAGAAATTATTTGG	354
Db	330	TTACGATTTTATTCATGTAAAGATTAAGATGGCATTCAAGAAACAGAGATTATTAATAG	389
OY	355	GAGGTTTTTCAGGAGAGAGACTTATCTTATATPACTGGCCCTTACCACAGACAGAAAC	414
Db	380	GAGGATTTCTATGGAGAGATGACATGGCAATGCATTAGCATATAGAAATCATCAAGATG	448
OY	415	TGGCAGGTGCATCCATCACTAGTTTCTTGCT	445
Db	450	TGGCAGGATATTGCTCTTTCTCAAGTTTCT	480

```

? RESULT 14
? US-09-853-386-88/c
? Sequence 88, Application US/09853386
? Patent No. US20020049151A1
? GENERAL INFORMATION:
? APPLICANT: Murphy, Evelyn
? APPLICANT: Bresnihan, Barry
? APPLICANT: Conneely, Orla
? APPLICANT: Fitzgerald, Oliver
? TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
? TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
? FILE REFERENCE: P01972US1
? CURRENT APPLICATION NUMBER: US/09/853,386
? CURRENT FILING DATE: 2001-05-11
? PRIOR APPLICATION NUMBER: US 60/203645
? PRIOR FILING DATE: 2000-05-12
? NUMBER OF SEQ ID NOS: 153
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 88
? LENGTH: 396
? TYPE: DNA
? ORGANISM: HUMAN
? US-09-853-386-88

```

Query Match	5.14	Score 36	DB 10	Length 396
Best Local Similarity	55.68	Pred. No. 0.2		
Matches	69	Conservative	0	Mismatches 55; Indels 0; Gaps
Qy	290	AAATATAAGCTTGTGATGATCAAGAAGTCAAGATGCAATCCCTTCTTAACAGAAATTAT	345	
Db	193	AAACATTAAACTCTCTCTGACACATTAAGAAATTAGATGTTCCGGGGCATTAATTCAA	136	
Qy	350	TTTGGAGGCTTTTCTCAGAGGAGAGCTTTTATCTTTATATATCTGCGCTTACCACACAGCA	405	
Db	133	TTAGGATGCTCTCAGAGGTCGCTTAAATATGTAATAATGCGCATTTCCATACAGAC	74	
Qy	410	GAAG	413	
Db	73	TAAA	70	

RESULT 15
US-09-321-987B-1

```
; Sequence 1, Application US/09321987B
; Patent No. us20020102210A1
; GENERAL INFORMATION:
; APPLICANT: Kimble, Judith E
; APPLICANT: Bluelloch, Robert H
; TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
; FILE REFERENCE: 960296.95386
; CURRENT APPLICATION NUMBER: US/09/321,987B
; CURRENT FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,170
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/129,023
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6659
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6450)
; US-09-321-987B-1
```

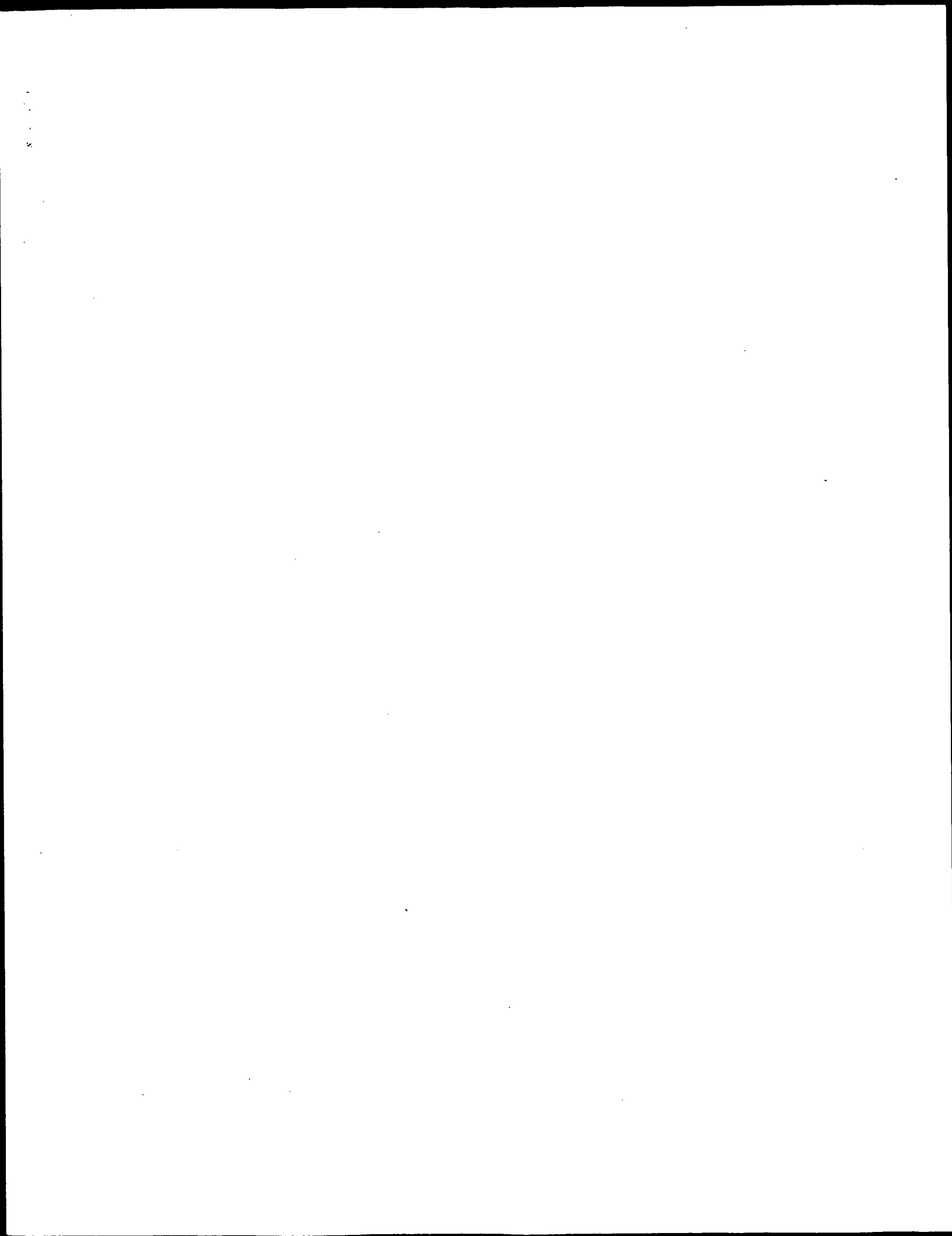
```
Query Match          5.0%; Score 35.6; DB 10; Length 6659;
Best Local Similarity 54.6%; Pred.No.1.5;
Matches 71; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 222 TGGTTGATATTATTTGGGCTTTCACACAGATTCACAGAGATGAATCGGATTAACAG 281
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 5752 TGTTTGAAGAAGTAATGCTCCGTCACACTGTGCAGAGCTTAATCAGATGTTAG 5811

QY 282 GCAGCAGAAATATATAAGCTTGTGATGATCAAGAAAGTGAAGATGGCATTCTTCTAAC 341
    || ||| | | | | | | | | | | | | | | | | | | | | | | | |
DB 5812 GCTAAAGATGCAATTAACATATCTCTTGACGGAATTCACCTAATGAATTTATGTCAT 5871

QY 342 AGAATTATTT 351
    ||| | | |
DB 5872 CGAATGAATT 5881
```

Search completed: January 19, 2003, 03:17:15
Job time : 111 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd

OM nucleic - nucleic search, using sw model

```
Run on:      January 19, 2003, 01:34:00 ; Search time 2230 Seconds
              (without alignments)
              5149.148 Million cell updates/sec
```

Title: US-09-988-982-2
Perfect score: 709
Sequence: 1 GCCGCTGCACGCCCTTGGG.....CAATTGATTGACGTCACTA 709

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

```
Searched:      1615406 segs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132
```

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	583.6	82.3	796	9	AUI32495	AUI32495 AUI32495
2	580.4	81.9	919	12	BS696407	BS696407 602658507
3	577.4	81.4	774	9	AUI30373	AUI30373 AUI30373
4	566	80.3	765	12	BS722409	BS722409 602693643
5	563	79.4	740	12	BS77497	BS77497 602720223
6	563	79.4	1061	13	BM475259	BM475259 AGENECOURT

7	563	79.4	1088	13	BM465006
8	561	79.1	1300	11	AF077199
9	559.4	78.9	1348	11	AF077198
10	559	78.8	796	10	BE618034
11	558.4	78.8	885	12	BG614082
12	557.6	78.6	711	13	BE150895
13	550.4	77.6	1042	13	BM558765
14	540.8	76.3	70501911	799	12
15	534.6	75.4	725	13	BE1596291
16	535.4	75.2	691	13	BE1906591
17	533.8	74.9	853	13	BE1494794
18	531.2	74.9	1162	12	BE8820266
19	530.8	74.3	889	14	BO227373
20	526.8	74.9	549	14	BM828718
21	523	73.8	896	12	BG528464
22	512.4	72.3	836	12	BG528464
23	512.4	72.3	931	12	BF970655
24	511.8	72.2	825	12	BG721347
25	509.2	71.8	739	13	BG615693
26	507.2	71.5	1050	12	BG166647
27	503.8	71.1	967	13	BE1464867
28	503.4	71.0	768	13	BE1917857
29	503.2	71.0	838	10	AV757844
30	503.2	71.0	898	12	BG6133559
31	502.4	70.9	698	12	BG28835
32	502.2	70.8	696	9	AU1278837
33	500	70.5	804	13	BE1562484
34	497.6	70.2	758	13	BE1560918
35	491	69.3	821	14	BO440078
36	485	68.4	1161	12	BM457120
37	483.4	68.2	734	12	BG433925
38	480.6	67.8	895	12	BE314398
39	477.2	67.5	640	12	BE545991
40	474.8	67.3	749	13	BE1827498
41	471.8	66.5	896	12	BG033014
42	466.4	65.8	485	9	AA436321
43	458.4	64.7	467	9	AA262396
44	454	64.0	621	10	AV713685
45	448.4	63.2	868	12	BG394007
					BM465006
					AGENCOURT
					AF077199
					Homo sapi
					AF077198
					Homo sapi
					BE618034
					60214623392
					BG614082
					602641734
					BE150895
					603195310
					BE150895
					603195310
					BM558765
					AGENCOURT
					BE501911
					602548224
					BE1596291
					602343007
					BE1906591
					603064126
					BE1549474
					603192140
					BE8820266
					601505311
					BO227373
					AGENCOURT
					BM828718
					K-EST0101
					BG528464
					602579913
					BE970655
					602273811
					BF971245
					602694890
					BG615693
					602643058
					BE1465556
					603203696
					BG166847
					602345021
					BE1464867
					603205930
					BE1917857
					603183987
					AV757844
					AV757844
					BG6133559
					602641906
					BG28835
					602405938
					AU127837
					AU127837
					BE1562484
					603263932
					BE1560918
					603254301
					BO440078
					AGENCOURT
					BM457120
					AGENCOURT
					BG433925
					AV7497218
					BE314398
					601901151
					BE545991
					602573290
					BE1827498
					603073944
					BG033014
					602300120
					AA436321
					zv22f06.r
					AA262396
					zs1608.r
					AV713685
					AV713685
					BG394007
					602415420

ALIGNMENTS

	RESULT 1
LOCUS	AU132495
DEFINITION	AU132495 796 bp mRNA linear EST 01-AUG-2000 AU132495 NT2RP3 Homo sapiens CDNA clone NT2RP3004603 5', mRNA sequence.
ACCESSION	AU132495
VERSION	AU132495.1
KEYWORDS	GI:10992849
SOURCE	EST.
ORGANISM	human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (Bases 1 to 796)
AUTHORS	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
TITLE	HRI human CDNA project
JOURNAL	Unpublished (2000)
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel.: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human CDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES	Location/Qualifiers
source	1. .796

```

/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT      191 a      188 c      196 g      214 t
ORIGIN           7 others

```

RESULT 2				
BG696407				
LOCUS	919 bp	mRNA	linear	EST 07-MAY-2001
BG696407				

DEFINITION	6026695053F1 NC1_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802053
ACCESSION	EG696407
VERSION	EG696407.1 GI:13961520
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

BASE COUNT	241 a	202 c	212 g	264 t	
ORIGIN					
Query Match		81.9%;	Score 580.4;	DB 12;	Length 919;
Best Local Similarity		90.4%;	Pred. No. 4.3e-162;		
Matches 657;	Conservative	1;	Mismatches 3;	Indels 66;	Gaps 1
OY	49	GCTTGCCCTGTGAGCTGAGCGCGGTGATGTTGGGGCAATATACATGTCACCCCGCTGCCG	108		
Db	1	GCTTGCCCTGTGAGCTGAGCGCGGTGATGTTGGGGCAATATACATGTCACCCCGCTGCCG	60		
OY	109	CCATCGTGGCCGCGCCCGGAAGCCACCGCTGCGGTATTTTCCGTCATGGATTGGAG	168		
Db	61	CCATCGTGGCCGCGCCCGGAAGCCACCGCTGCGGTATTTTCCGTCATGGATTGGAG	120		
OY	169	ATACTGG-----	175		
Db	121	ATACTGGGCAAGGATGGGCGAGAGCCTTTCAGAGTATCAGAGTTACATATCAATAATA	180		
OY	176	-----GCTGTAGGCGCTGTTACATTTAAATATGACGTGCTATGCTTCAT	222		
Db	181	TCTGCCGCAATGGCCCTGTAGGCTGTATACATTTAAATATGACGTGCTATGCTTCAT	240		
OY	223	GGTTGATATTTATGGGCTTTCACACGATTCACAGAGAGATGAACTGGGTTAAACAG	282		
Db	241	GGTTGATATTTATGGGCTTTCACACGATTCACAGAGAGATGAACTGGGTTAAACAG	300		
OY	283	CAGCAGAAATATTAAGCTTTGATGATCAGAAAGTGAAAGTGGATTCCTCTTACA	342		
Db	301	CAGCAGAAATATTAAGCTTTGATGATCAGAAAGTGAAAGTGGATTCCTCTTACA	360		
OY	343	GAAATATTTTGGAGGGTTTTCACAGGAGAGCTTATCTTATATACCTGCCCTTACA	402		
Db	361	GAAATATTTTGGAGGGTTTTCACAGGAGAGCTTATCTTATATACCTGCCCTTACA	420		
OY	403	CACAGCAGAAATCGCAGGTGTCTACTGCACATGATTTCTTGCTTCCACTTGGGNTTCT	462		
Db	421	CACAGCAGAAATCGCAGGTGTCTACTGCACATGATTTCTTGCTTCCACTTGGGNTTCT	480		

OY	463	TTCCACAGGKCCCTTTCGCTGCTTATPAGAGATATTTCATTTCACAGTCCACGGGG	522
Db	461	TTCCACAGGGTCCTATCGGTGCTTAATAGAGATATTTCATTTCACAGTCCACGGGG	540
OY	523	ATTGTGACCCCTTTGGTTCCTCGATGTTTGGTTCCTTAACGGTGGAAAAACCTAAAAACAT	582
Db	541	ATTGTGACCCCTTTGGTTCCTCGATGTTTGGTTCCTTAACGGTGGAAAAACCTAAAAACAT	600
OY	583	TGGTAAATCCAGCCCAATGTGACCTTTAAACCTATGAAAGTATGATGACATTTGGTGTG	642
Db	601	TGGTAAATCCAGCCCAATGTGACCTTTAAACCTATGAAAGTATGATGACATTTGGTGTG	660
OY	643	AACAGAAATGATGATGTCAAGCAATTCATTGATGAACTCCTACCTCCAAATGATTGAC	702
Db	661	AACAGAAATGATGATGTCAAGCAATTCATTGATGAACTCCTACCTCCAAATGATTGAC	720
OY	703	GTCACTA 709	
Db	721	GTCACTA 727	

RESULT 3				
AUI33073				
LOCUS	774 bp	mRNA	linear	EST 01-AUG-2002
DEFINITION	AUI33073	NT2RP4	Homo sapiens	CDNA clone NT2RP4001208 5', mRNA
ACCESSION	Sequence.	AUI33073		
VERSION	AUI33073.1	GI:10993612		
KEYWORDS	EST.			
SOURCE	human.			

REFERENCE
AUTHORS
Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y., Saito, K., Yamamoto, J.,
Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 774)

TITLE

JOURNAL
COMMENT
Unpublished (2000)
Contact: Takao Isogai

Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kiserazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES	Location/Qualifiers
source	1. .774

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP4001208"
/clone_1lb="NT2RP4"
/cell_type="teratocarcinoma"
/cell_line="NP2"
/note="Vector: pME18SFL3; mRNA from NP2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT
197 a 173 c 185 g 216 t 3 others

```

Query Match	81.4%;	Score 577.4;	DB 9;	Length 774;
Best Local Similarity	90.2%;	Pred. NO. 3.2e-16;		
Matches 665; Conservative	1;	Mismatches 4;	Indels 67;	Gaps 2;

QY 40 CTTCCTCCGCTTGCGCTGTAGCTGAGCGGGTATGTGCGGCAATACATGTCAACC 99
|||||
Dd 1 CTTCCTCCGCTTGCGCTGTAGCTGAGCGGGTATGTGCGGCAATACATGTCAACC 60

OY	100	CGCTGCGCGGCATCTGTGCGCCGCGCGCCGGAAGGCCACCGCTGCGGTGATTTTCTCTGATG	159
Db	61	CGCTGCGCGGCATCTGTGCGCCGCGCGCCGGAAGGCCACCGCTGCGGTGATTTTCTCTGATG	120
OY	160	GATTGGAGATGATCTGCG-----	175
Db	121	GATTGGAGATGATCTGCGCGACGCGATGGGCGAAGAACCTTTTCAGGTATCAGAACTTCACATA	180
OY	176	-----GCTGTGTAGGCGCTGTTCATTTAATTAATGAACGTGGCTA	213
Db	181	TCAATATATCTGCGCGCGATGGCGCGCTGTAGGCGCTGTTCATTTAATTAATGAACGTGGCTA	240
OY	214	TGCTTTTCATGCTTTATATATTTATTTGGGCTTTCACACAGATTCACACGAGATGTAATCTGGGA	273
Db	241	TGCTTTTCATGCTTTATATTTATTTGGGCTTTCACACAGATTCACACGAGATGTAATCTGGGA	300
OY	274	TTAAACAGGCGACCAAAAAATATAAAGCTTTGATTTGATTCACAAAGCAGAAATGGCATTC	333
Db	301	TTAAACAGGCGACCAAAAAATATAAAGCTTTGATTTGATTCACAAAGCAGAAATGGCATTC	360
OY	334	CTTTCACAGAAATTTATTTTGGGAGGCTTTTCACAGGAGAGACTTATTTATATATCTG	393
Db	361	CTTTCACAGAAATTTATTTTGGGAGGCTTTTCACAGGAGAGACTTATTTATATATCTG	420
OY	394	CCCTTACACACAGCAGAAACTGGCAGGTGTCACCTGACCTAGTTTCTTGCCTTCACCTTC	453
Db	421	CCCTTACACACAGCAGAAACTGGCAGGTGTCACCTGACCTAGTTTCTTGCCTTCACCTTC	480
OY	454	GCGATTTCTTTCCACAGGAGKCTATTCGGTGTGCTTAATAGATATTTTCTATTTCTCACT	513
Db	481	GCGATTTCTTTCCACAGGAGKCTATTCGGTGTGCTTAATAGATATTTTCTATTTCTCACT	540
OY	514	GCCACGGGGATTTGTACCCCTTTGGTCCCGCTATGTTTGGTCTCTGTACGGTGAAGAAAC	573
Db	541	GCCACGGGGATTTGTACCCCTTTGGTCCCGCTATGTTTGGTCTCTGTACGGTGAAGAAAC	600
OY	574	TAAAAACATTTGGTGAATCCAGCCAAATGTGACTTTTAAAAACCTTAAGGATATGATGACAC-	632
Db	601	TAAAAACATTTGGTGAATCCAGCCAAATGTGACTTTTAAAAACCTTAAGGATATGATGACACA	660
OY	633	AGTTGCTGTCAACAGGAAATGATGGATGTGCAAGCAATTCATTTGATTAACCTCTACTCCCA	692
Db	661	AGTTGCTGTCAACAGGAAATGATGGATGTGCAAGCAATTCATTTGATTAACCTCTACTCCCA	720
OY	693	ATTGATTTGACGTCACTA 709	
Db	721	ATTGATTTGACGTCACTA 737	

RESULT 4	LOCUS	DEFINITION
BG722409	BG722409	602693642F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4825691 5', mRNA sequence.

ACCESSION	BG722409
VERSION	BG722409.1
KEYWORDS	EST.
SOURCE	human.

ORGANISM Homo sapiens
Eukaryotes: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
1 (bases 1 to 765)
NIH-MGC <http://mgc.ncl.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihrakhi Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM10739 row: d column: 12
High quality sequence stop: 712.

FEATURES	Location/Qualifiers
source	1. .765

BASE COUNT ORIGIN	179 a	187 c	195 g	204 t
----------------------	-------	-------	-------	-------

ORIGIN

Query Match	80.3%;	Score 569;	DB 12;	Length 765;
Best Local Similarity	89.3%;	Pred. No. 1e-158;		
Matches 673;	Conservative	1;	Mismatches 12;	Indels 68;
				Gaps 3;

OY	1	GCCTGTCACAGCCCTTGGGCGCGGGCGGGCGCCGCTTCCTTCCTTCGCGCTGGCGTG	60
Db	10	GCCGCTGCACAGCCCTTGGGCGCGGGCGGGCGCCGCTTCCTTCCTTCGCGCTGGCG	69
OY	61	AGCTAGCGCGGTGTATGTGCGGCATTAACTGTCAACCCCGCTGCCCGGCATCGTGGCCG	120
Db	70	AGCTAGGCGGTGTATGTGCGGCATAATGTCAACCCCGCTGCCCGGCATCGTGGCCG	129
OY	121	CCGCCCGGAAGGCCACCCGCTGCGGTGATTTTCTCGATGGATTGGAGATPACG----	175
Db	130	CCGCCCGGAAGGCCACCCGCTGCGGTGATTTTCTCGATGGATTGGAGATPACGCGACG	189
OY	176	-----	175
Db	190	GATGGCAGAAACCTTTCGAGGTATCGAAGTTCACATATCAAAATATATCGCCGCA	249
OY	176	-GCGTGTAGGCGCTGTATCAATTAATATGAAAGTGGCTATGCCCTCATGGTTGATATTA	234
Db	250	CGCCTGTTAGGCGCTGTATCAATTAATATGAAAGTGGCTATGCCCTCATGGTTGATATTA	309
OY	235	TTGGGCTTTCACAGATTCACAGAGGATGAATCTGGGATTAAACAGCGACAGAAATA	294
Db	310	TTGGGCTTTCACAGATTCACAGAGGATGAATCTGGGATTAAACAGCGACAGAAATA	369
OY	295	TAAAGCTTTGATTTGATTCAGAAAGTAAGAAATGGCAATTCCTTCTTAACAGAAATTTTGG	354
Db	370	TAAAGCTTTGATTTGATTCAGAAAGTAAGAAATGGCAATTCCTTCTTAACAGAAATTTTGG	429
OY	355	GAGGTTTTCTCAGGGAGGAGCTTATATCTTATATCTGCCCTTACCACACAGCAGAAAC	414
Db	430	GAGGTTTTCTCAGGGAGGAGCTTATATCTTATATCTGCCCTTACCACACAGCAGAAAC	489
OY	415	TGGCAGGTCTCACTGCACACAGTTTCTTCCCTCACTTGGGGTTCCTTCCACAGGAC	474
Db	490	TGGCAGGTCTCACTGCACACAGTTTCTTCCCTCACTTGGGGTTCCTTCCACAGGAC	549
OY	475	CTATCGGTGTGCTAATTAAGATATTTCTCACTCCAGTGCACAGGGGATTTGACCTT	534
Db	550	CTATCGGTGTGCTAATTAAGATATTTCTCACTCCAGTGCACAGGGGATTTGACCTT	609
OY	535	TGGTTCCCTGATGTTTGGTTCTTTACGGTGGAAAACTAAAAACATTGGTGAATCAG	594
Db	610	TGGTTCCCTGATGTTTGGTTCTTTACGGTGGAAAACTAAAAACATTGGTGAATCAG	668
OY	595	CCAATGTACCTTTAAACCTAAGAAGTATGATGCAAGTTCGTGTCAACAGAAATGA	654

Db 669 CCATGTGCCTTTTAAACCTATGAGTATGATGCACAGTGTGTATCAGAGAAACTGA 728

Qy 655 TGA-TGTCAAGCATTCATTGATTAACCTCTAC 687

Db 729 TGGACGTCAAGCATTCCTCGATTAACCTCTAC 762

RESULT	5
B6773497	
LOCUS	
DEFINITION	740 bp mRNA linear EST 15-MAY-2001 602720223F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4837420 5 , mRNA sequence.
ACCESSION	B6773497
VERSION	BG773497.1 GI:14084150
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

FEATURES	Location/Qualifiers
source	1. .740

BASE COUNT	168 a	179 c	197 g	196 t
ORIGIN				

Query Match	79.4%;	Score 563;	DB 12;	Length 740;
Best Local Similarity	89.7%;	Pred. No. 6.2e-157;		
Matches 642; Conservative	1;	Mismatches 7;	Indels 66;	Gaps 1

QY	1	GGCGCTGCGACGGCCCTTTGGGCGCGGGCGCCCGCTTTCCTTCCGCTGTCGGCTGTG	60
Db	23	GCCGCTTCGACAGCCCTTTGGGCGCGGGCGCCCGCGCTTTCCTTCCGCTTCCGCTGTG	82
QY	61	AGCTGAGGCGGTGTATGTGGCGGCATTAACATGTCAACCCCGCTGCCCGCATGTGCCG	120
Db	83	AGCTGAGGCGGTGTATGTGGCGGCATTAACATGTCAACCCCGCTGCCCGCATGTGCCG	142
QY	121	CCGCGCGGAAGGCCACCGCTGCGCGGTGATTTTCTCGATGATTTGGGAGATACACG	175
Db	143	CCGCGCGGAAGGCCACCGCTGCGCGGTATTTTCTCGATGATTTGGGAGATACGCGACG	202
QY	176	-----	175

Db 203 GATGGCAGAGACCTTTGAGGTATCAGAAAGTTCATATCATATATATCTGCCGATG 262
 QY 176 -GCTGTAGGCTGTATCATTAATATGAAGCTATGCTATGCTCATGTTTGAATTA 234
 Db 263 CGCTGTATAGGCTGTATCATTAATATGAAGCTATGCTATGCTCATGTTTGAATTA 322
 QY 235 TTGGGCTTTACACAGATTTCACAGAGAGATGAATCTGGATTAAACAGCAGAGAAAATA 294
 Db 323 TTGGGCTTTACACAGATTTCACAGAGAGATGAATCTGGATTAAACAGCAGAGAAAATA 382
 QY 295 TAAAGCTTTGATATCATGAAGAAGATGATGATCTTCTTACGAAATTTTGG 354
 Db 383 TAAAGCTTTGATATCATGAAGAAGATGATGATCTTCTTACGAAATTTTGG 442
 QY 355 GAGGCTTTCTCAGGAGAGCTTATCTTATATACGCTTACACAGAGAGAAAC 414
 Db 443 GAGGCTTTCTCAGGAGAGCTTATCTTATATACGCTTACACAGAGAGAAAC 502
 QY 415 TGGCAGGTGTCACTGCTCATGTTCTTGTCTTCCACTTGGGNTTCTTTCACAGAGGC 474
 Db 503 TGGCAGGTGTCACTGCTCATGTTCTTGTCTTCCACTTGGGNTTCTTTCACAGAGGC 562
 QY 475 CTATGGGTGTCTATATGAGATATTTCTATTTCTTCCACTGCGCAGGGGATTTGACCTT 534
 Db 563 CTATGGGTGTCTATATGAGATATTTCTATTTCTTCCACTGCGCAGGGGATTTGACCTT 622
 QY 535 TGGTCCCTGATGTTTGTCTCTTACGCTGAGAAACATTAACATTTGTAATCCAG 594
 Db 623 TGGTCCCTGATGTTTGTCTCTTACGCTGAGAAACATTAACATTTGTAATCCAG 682
 QY 595 CCAATGTACCTTTAAACCTATGAAAGTATGATGACAGAGTGTCTTCAACAGGAA 650
 Db 683 CCAATGTACCTTTAAACCTATGAAAGTATGATGACAGAGTGTCTTCAACAGGAA 738

RESULT 6
 BM475259 1061 bp mRNA linear EST 05-FEB-2002
 LOCUS AGENCOURT_6477939 NIH_MGC_67 Homo sapiens cdna clone IMAGE:5578672
 DEFINITION 5', mRNA sequence.
 ACCESSION BM475259
 VERSION BM475259.1 GI:18524301
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1061)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: gsa@f5email.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLAM2334 row: b column: 17
 High quality sequence stop: 618.

FEATURES

Location/Qualifiers
 1..1061
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5578672"
 /clone_lib="NIH_MGC_67"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site: 1: Not; Site: 2: SalI; cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life

Technologies."
 BASE COUNT 281 a 228 c 229 g 319 t 4 others
 ORIGIN

Query Match 79.4%; Score 563; DB 13; Length 1061;
 Best Local Similarity 89.5%; Pred. No. 7.1e-157;
 Matches 642; Conservative 1; Mismatches 8; Indels 66; Gaps 1;

QY 59 TGACCTAGAGCGGTGTATGTGCGGCATTAACATGTCACACCCCGCTGCCCATCGTGC 118
 Db 1 TGACCTAGAGCGGTGTATGTGCGGCATTAACATGTCACACCCCGCTGCCCATCGTGC 60
 QY 119 CGCGCCCGGAGAGCCACCGCTGCGGTGATTTTCTCATGATTTGGAGATCTGG--- 175
 Db 61 CGCGCCCGGAGAGCCACCGCTGCGGTGATTTTCTCATGATTTGGAGATCTGGGCA 120
 QY 176 ----- 175

Db 121 CGATGGGCAAGACCTTTGACGATTCAGAAAGTTCATATCATATATATCTGCCGCA 180
 QY 176 ---GCTGTAGGCTGTATCATTAATATGAAGCTATGCTATGCTCATGTTTGAAT 232
 Db 181 TGGCCTGTATAGGCTGTATCATTAATATGAAGCTATGCTATGCTCATGTTTGAAT 240
 QY 233 TATGGCTTTACACAGATTTCACAGAGAGATGATCTGGGATTAAACAGCAGAGAA 292
 Db 241 TATGGCTTTACACAGATTTCACAGAGAGATGATCTGGGATTAAACAGCAGAGAA 300
 QY 293 TATAAAGCTTTGATATGATCAAGAGTGAAGTGGCATTCCTTCAACAGAAATTA 352
 Db 301 TATAAAGCTTTGATATGATCAAGAGTGAAGTGGCATTCCTTCAACAGAAATTA 360

QY 353 GGGAGGTTTTCTCAGGAGAGAGCTTATGTTTATATACGCTTACACAGAGAGAA 412
 Db 361 GGGAGGTTTTCTCAGGAGAGAGCTTATGTTTATATACGCTTACACAGAGAGAA 420
 QY 413 ACTGGAGGTGTCACTGCTCATGTTCTTGTCTTCCACTTGGGNTTCTTTCACAGAG 472
 Db 421 ACTGGAGGTGTCACTGCTCATGTTCTTGTCTTCCACTTGGGNTTCTTTCACAGAG 480

QY 473 KCCTATCGGTGTCTATATGAGATATTTCTATTTCTTCCACTGCGCAGGGGATTTGACCC 532
 Db 481 TCCATCGGTGTCTATATGAGATATTTCTATTTCTTCCACTGCGCAGGGGATTTGACCC 540
 QY 533 TTTGGTCCCTGATGTTTGTCTCTTACGCTGAGAAACCTAAACATTTGTAATCC 592
 Db 541 TTTGGTCCCTGATGTTTGTCTCTTACGCTGAGAAACCTAAACATTTGTAATCC 600

QY 593 AGCCAATGTACCTTTAAACCTATGAAAGTATGATGACAGTGTCTTCAACAGAGAA 652
 Db 601 AGCCAATGTACCTTTAAACCTATGAAAGTATGATGACAGTGTCTTCAACAGAGAA 660
 QY 653 GATGATGTCAACCAATTCATTAATCTCTTCACTCCAAATTTGATGACGTCAC 709
 Db 661 GATGATGTCAACCAATTCATTAATCTCTTCACTCCAAATTTGATGACGTCAC 717

RESULT 7
 BM465006 1088 bp mRNA linear EST 05-FEB-2002
 LOCUS AGENCOURT_6428540 NIH_MGC_85 Homo sapiens cdna clone IMAGE:5505154
 DEFINITION 5', mRNA sequence.
 ACCESSION BM465006
 VERSION BM465006.1 GI:18514048
 KEYWORDS EST.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1088)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: c9apds-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LLM12147 row: k column: 11
 High quality sequence stop: 563.
 Location/Qualifiers

FEATURES

source

1. 1088
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:505154"
 /clone_1ib="NIH_MGC_85"
 /issue_type="Lymphoma, cell line"
 /lab_host="PH10B (phage-resistant)"
 /note="Organ: Lymph. Vector: PCMV-SPORE6; Site:1: NotI;
 Site:2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.867 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."
 BASE COUNT 255 a 300 c 225 g 306 t 2 others
 ORIGIN

Query Match

Best Local Similarity 89.5%; Score 563; DB 13; Length 1088;
 Matches 664; Conservative 1; Mismatches 9; Indels 68; Gaps 3;

34 CCGGCTTCCTCCGCTGCTGAGTGAAGGCGGTATGTCGGCAATACATG 93
 1 CTTGCTCTCTCCCTGCTGCTGAGTGAAGGCGGTATGTCGGCAATACATG 60
 94 CAACCCCGCTGCGCCGATGTCGCCGCCGCGGAAGGCCACGCTGGGATTTCC 153
 61 CAACCCCGCTGCGCCGATGTCGCCGCCGCGGAAGGCCACGCTGGGATTTCC 120
 154 TGCATGATGCGAGATACG----- 175
 121 TGCATGATGCGAGATACGAGATGCGAGAGAGCTTTGAGATGAGATG 180
 176 -----GCCGTGAGCTGTTACATTAATATGAGC 207
 181 CACATATCAATATATGTCGCCGATGCGCTGTTAGCCTGTTACATTAATATGAGC 240
 208 TGGCTATGCTTATGTTGATATTTGGCTTTCCACAGATTCACAGAGATGAT 267
 241 TGGCTATGCTTATGTTGATATTTGGCTTTCCACAGATTCACAGAGATGAT 300
 268 CTGGGATTAACAGCGCAGAAATTAACCTTGATGATCAAGAAAGTAAAG 327
 301 CTGGGATTAACAGCGCAGAAATTAACCTTGATGATCAAGAAAGTAAAG 360
 328 GCATTCCTTCAAGATATTTGGAGGTTTCTCAGAGAGAGCTTTATCTTAT 387
 361 GCATTCCTTCAAGATATTTGGAGGTTTCTCAGAGAGAGCTTTATCTTAT 420
 388 ATATGCTTACACACAGCAAACTGAGGTGCTACATGCACTGATTTTCTTC 447
 421 ATATGCTTACACACAGCAAACTGAGGTGCTACATGCACTGATTTTCTTC 480
 448 CACTTGGGNTTCTTCCACAGGKCTATGCTGCTATAGAGATATTTCTATTC 507
 481 CACTTGGGNTTCTTCCACAGGKCTATGCTGCTATAGAGATATTTCTATTC 540
 508 TCCAGTCCACAGGATTTGACCTTTGGTTCCCTGATGTTGTTCTTACGATG 567
 541 TCCAGTCCACAGGATTTGACCTTTGGTTCCCTGATGTTGTTCTTACGATG 600
 568 AAAAACTAAAACTGGTGAATCCAGCAATGATGACCTTAAACCTATGAAGATGA 627

Db 601 AAAAACTAAAACTGGTGAATCCAGCAATGATGACCTTAAACCTATGAAGATGA 660
 Qy 628 TCCAGTCCACAGGATTTGACCTTTGGTTCCCTGATGTTGTTCTTACGATG 687
 Db 661 TCCAGTCCACAGGATTTGACCTTTGGTTCCCTGATGTTGTTCTTACGATG 719
 Qy 688 CTCCATGATGATGACGTCACCTA 709
 Db 720 CTCC-ATTGATGATGACGTCCTTA 740

RESULT 8

AF077199 1300 bp mRNA linear HTC 22-MAY-2001
 LOCUS Homo sapiens Lysophospholipase Isoform mRNA, complete cds.
 DEFINITION AF077199
 ACCESSION AF077199.1 GI:4679011
 VERSION AF077199.1 GI:4679011
 KEYWORDS HTC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1300)
 Zhang, Q.H., Ye, M., Wu, X.Y., Ren, S.X., Zhao, M., Zhao, C.J., Fu, G.,
 Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W.,
 Tao, J., Huang, Q.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J., and Chen, Z.
 Cloning and functional analysis of cDNAs with open reading frames
 for 300 previously undefined genes expressed in CD34+ hematopoietic
 stem/progenitor cells

TITLE

JOURNAL MEDLINE
 PUBMED
 11042152
 2 (bases 1 to 1300)
 Shen, Y., Guan, Z., Gu, J., Ye, M., Zhou, J., Zhang, Q., Xu, S., He, K.,
 Chen, S., Mao, M. and Chen, Z.
 Human Lysophospholipase gene(short form)
 Unpublished

JOURNAL

Submitted (10-JUL-1998) Shanghai Institute of Hematology, Shanghai
 Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
 Shanghai 200025, P. R. China
 Location/Qualifiers

FEATURES

source
 1. 1300
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="CD34+ cell"
 6. 650
 /codon_start=1
 /product="Lysophospholipase isoform"
 /protein_id="AAD26994.1"
 /db_xref="GI:4679012"

CDS

/translation="MCGNNMSTPLPAIVPAARKTAIVFLHIGDTHGMAEAFAGI
 RSSHRTICPHAFDITGLSPDSODESGIKOAAHNTALIDQPKRNPISNRITLGSF
 SQGALSILYTLATYQKLAGYALSCWPLPAASPQPGIGANADISILDCGHCDFL
 VPLMGSTVTEKLTILVPAWVETKTEGMHSSCOEDMDVYKOFIDKLPLPD"

BASE COUNT

381 a 246 c 254 g 419 t
 Query Match 79.1%; Score 561; DB 11; Length 1300;
 Best Local Similarity 92.2%; Pred. No. 3e-156;
 Matches 607; Conservative 1; Mismatches 32; Indels 18; Gaps 1;

Qy 70 GGTATGATGGGCGCATATACATGTCACCCGCTCCGCCATCTGCGCCGCCGCGA 129
 Db 1 GGTATGATGGGCGCATATACATGTCACCCGCTCCGCCATCTGCGCCGCCGCGA 60
 Qy 130 AGGCCACCGCTCGGATTTTCTGATGATTTGGAGATATGAGGCTGTTAGCCTG 189
 Db 61 AGGCCACCGCTCGGATTTTCTGATGATTTGGAGATATGAGGCTGTTAGCCTG 120
 Qy 190 TTACATTT-----AAATATGACAGCTGCTATGCTTCATGTTTGAATA 231

```

Db 121 AAGCCTTGCAGGATCAGAGTTCACATATCAATATATCTGCGCCGATCGTTGATA 180
QY 232 TTATGGGCTTTCACACAGATTCACAGAGATGAACTGGATTAACAGGACAGAGAA 291
Db 181 TTATGGGCTTTCACACAGATTCACAGAGATGAACTGGATTAACAGGACAGAGAA 240
QY 292 ATATAAAGCTTGTATGATCAAGAGTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 351
Db 241 ATATAAAGCTTGTATGATCAAGAGTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 300
QY 352 TGGAGGGTTCCTCAGAGGAGAGCTTATCTTATATCTGCGCCCTTACACAGAGAGA 411
Db 301 TGGAGGGTTCCTCAGAGGAGAGCTTATCTTATATCTGCGCCCTTACACAGAGAGA 360
QY 412 AACTGGCAGGTGTACCTGCTAGCTGCTTCTGCTTCCACTTCCGAGGNTTCTTCCAGAG 471
Db 361 AACTGGCAGGTGTACCTGCTAGCTGCTTCTGCTTCCACTTCCGAGGNTTCTTCCAGAG 420
QY 472 GKCCATGCGTGTGCTAATAGATATTTCTATCTTCCAGTGGCAGGGGATTTGACC 531
Db 421 GTCCATGCGTGTGCTAATAGATATTTCTATCTTCCAGTGGCAGGGGATTTGACC 480
QY 532 CTTTGGTCCCTGATGTTGTTGTTCTCTACGTGAGAAAACTAAAAACAATTGGTGAATC 591
Db 481 CTTTGGTCCCTGATGTTGTTGTTCTCTACGTGAGAAAACTAAAAACAATTGGTGAATC 540
QY 592 CAGCAATGTCATCTTAAACCTATGAGATGATGACAGAGTCTGTCACAGAGAAA 651
Db 541 CAGCAATGTCATCTTAAACCTATGAGATGATGACAGAGTCTGTCACAGAGAAA 600
QY 652 TGATGATGTCACCAATTCATGATTAACCTCACTCACTCAATGATGAGCTGACTA 709
Db 601 TGATGATGTCACCAATTCATGATTAACCTCACTCACTCAATGATGAGCTGACTA 658

```

```

RESULT 9
AF077198 1348 bp mRNA linear HTC 22-MAY-2001
LOCUS Homo sapiens lysophospholipase mRNA, complete cds.
DEFINITION AF077198.1 GI:4679009
VERSION Homo sapiens.
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1348)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Zhang, Q.H., Ye, M., Wu, X.Y., Ren, S.X., Zhao, M., Zhao, C.J., Fu, G.,
Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W.,
Tao, J., Huang, Q.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z.
Cloning and functional analysis of cDNAs with open reading frames
for 300 previously undefined genes expressed in CD34+ hematopoietic
stem/progenitor cells
JOURNAL Genome Res. 10 (10), 1546-1560 (2000)
MEDLINE 20493367
PUBMED 11042152
REFERENCE 2 (bases 1 to 1348)
AUTHORS Shen, Y., Guan, Z., Gu, J., Ye, M., Zhou, J., Zhang, O., Xu, S., He, K.,
Chen, S., Mao, M. and Chen, Z.
Human lysophospholipase gene
TITLE Unpublished
REFERENCE 3 (bases 1 to 1348)
AUTHORS Shen, Y.
JOURNAL Direct Submission
REFERENCE Submitted (10-JUL-1998) Shanghai Institute of Hematology, Shanghai
JOURNAL Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,
Shanghai 200025, P. R. China
FEATURES
source location/Qualifiers
1..1348
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="CD34+ cell"

```

```

CDS 5..698
/codon_start=1
/product="Lysophospholipase"
/protein_id="AAD2693.1"
/db_xref="GI:4679010"
/translation="MCGNMSRPLPAIVPARKATVAIFLHGLDTGHNAEAFAGI
RSSHIKVICPBAVPRPVTLNMYAMPSPMDIIGLSPPDSEDSSGKQAAENKALIDQ
EYKNGIPSRRIILGFSOGGALSLYLTALITTOOKLGLVYALSCWLPFRSFPDPIGA
NRDSTLQCHGDCDPLVPLMFSLIVELKTLVNPANVTFKYEGMHSSCQEQEMDV
KQFIDKLAPID"
BASE COUNT 392 a 256 c 265 g 435 t
ORIGIN
Query Match 78.9%; Score 559.4; DB 11; Length 1348;
Best Local Similarity 90.1%; Pred. No. 9, 2e-156;
Matches 636; Conservative 1; Mismatches 3; Indels 66; Gaps 1;
QY 70 GGTGTATGTGCGGCATTAACATGTCACACCCGCTGCGCCGATCGTCCGCGCGGGA 129
Db 1 GGTGTATGTGCGGCATTAACATGTCACACCCGCTGCGCCGATCGTCCGCGCGGGA 60
QY 130 AGGCCACCGCTGGGATTTTCTGCATGATGGAGATGAGTCTG----- 175
Db 61 AGGCCACCGCTGGGATTTTCTGCATGATGGAGATGAGTCTG----- 120
QY 176 -----GCTGTGA 183
Db 121 AAGCCTTGCAGGATTCAGAGTTCACATATCAATATATCTGCGCCGATGCGCCTGTTA 180
QY 184 GGCCTTACATTAATTAATGAAGCGTATGCTATGCTCATGTTGATTAATGGGCTTT 243
Db 181 GGCCTTACATTAATTAATGAAGCGTATGCTATGCTCATGTTGATTAATGGGCTTT 240
QY 244 CACCAATTCACAGAGAGATGAACTGGGATTAACAGCAGCAGAGAAAATATAAAGCTT 303
Db 241 CACCAATTCACAGAGAGATGAACTGGGATTAACAGCAGCAGAGAAAATATAAAGCTT 300
QY 304 TGATGATCAAGAGTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 363
Db 301 TGATGATCAAGAGTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 360
QY 364 CTCAGGAGAGAGCTTATCTTATATATCTGCTTACACAGCAGAGAACTGGCAGGTG 423
Db 361 CTCAGGAGAGAGCTTATCTTATATATCTGCTTACACAGCAGAGAACTGGCAGGTG 420
QY 424 TCACCTGCACTCACTTCTTCCACTTCCAGTGGGNTTCTTCCAGAGGKCTATCGGTG 483
Db 421 TCACCTGCACTCACTTCTTCCACTTCCAGTGGGNTTCTTCCAGAGGKCTATCGGTG 480
QY 484 GTGCTAATAGAGATTTCTTATCTTCCAGTGGCAGGAGATTTGACCTTTGGTTCGCC 543
Db 481 GTGCTAATAGAGATTTCTTATCTTCCAGTGGCAGGAGATTTGACCTTTGGTTCGCC 540
QY 544 TGATGTTGGTCTCTTACGAGTGAAGAACTAAAAACATTTGGTGAATCAGCAATGTA 603
Db 541 TGATGTTGGTCTCTTACGAGTGAAGAACTAAAAACATTTGGTGAATCAGCAATGTA 600
QY 604 CCTTAAACCTATGAGGTATGATGACAGATTCGTTGACACAGAGAAATGATGATGTA 663
Db 601 CCTTAAACCTATGAGGTATGATGACAGATTCGTTGACACAGAGAAATGATGATGTA 660
QY 664 AGCAATTCATGATTAACCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 709
Db 661 AGCAATTCATGATTAACCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 706
RESULT 10
BE618034 796 bp mRNA linear EST 20-OCT-2000
LOCUS 601462392P1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865775 5',
DEFINITION mRNA sequence.
ACCESSION BE618034
VERSION BE618034.1 GI:988972

```

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 796)
TITLE	NIH-MGC http://mgc.ncl.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaps@email.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.nih.gov Plate: L14M9609 row: 9 column: 24 High quality sequence stop: 694.
FEATURES	location/Qualifiers
source	1..796
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:3865775"
	/clone_1id="NIH.MGC.67"
	/tissue_type="retinoblastoma"
	/lab_host="DH10B (phage-resistant)"
	/note="Organ: eye; Vector: pCMV-SORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Life Technologies."
BASE COUNT	186 a 196 c 207 g 207 t
ORIGIN	
Query Match	78.8%; Score 559; DB 10; Length 796;
Best Local Similarity	88.0%; Pred. No.1e-155;
Matches 658; Conservative	1; Mismatches 22; Indels 67; Gaps 2;
QY	1 GCCGCTCGCACGCCCTTGGCGCGCGCGCGCGCGCGCTCTCTCCGCTTGCGCTGTG 60
Db	1 GCCGCTCGCACGCCCTTGGCGCGCGCGCGCGCGCGCTCTCTCCGCTTGCGCTGTG 60
QY	61 AGCTAGGCGGTGATGTGGCGCATATCAATGCAACCCCGTGGCGCGCATGTGCGCG 120
Db	61 AGCTAGGCGGTGATGTGGCGCATATCAATGCAACCCCGTGGCGCGCATGTGCGCG 120
QY	121 CGCGCCGGAAGGCACCCGCTCGGTGATTTTCCTCATGATGTGGAGATCTGG----- 175
Db	121 CGCGCCGGAAGGCACCCGCTCGGTGATTTTCCTCATGATGTGGAGATCTGGGCAG 180
QY	176 ----- 175
Db	181 GATGGCAGAAAGCCCTTTCAGGTATCAAGAAGTTCACATATCAAAATATCTGCCCGCATG 240
QY	176 -GCCGTAGAGCGCTTTCATTAATATGAACGCTGCTATGCGCTTCATGATTTGATATTA 234
Db	241 CGCCTGTAGGCGCTTTCATTAATATGAACGCTGCTATGCGCTTCATGATTTGATATTA 300
QY	235 TTGGGCTTTCACACAGATTCACAGAGAGATGTGGATTTAAACAGGCAGCAAAATA 294
Db	301 TTGGGCTTTCACACAGATTCACAGAGAGATGTGGATTTAAACAGGCAGCAAAATA 360
QY	295 TAAAGGCTTGTATATCAAGAAGTGAAGATGGCATTCCTTCAACGAATATATTGG 354
Db	361 TAAAGGCTTGTATATCAAGAAGTGAAGATGGCATTCCTTCAACGAATATATTGG 420
QY	355 GAGGCTTTCACAGAGAGAGCTTATCTTATATATACGCGCTTACACACAGCAGAAC 414
Db	421 GAGGCTTTCACAGAGAGAGCTTATCTTATATATACGCGCTTACACACAGCAGAAC 480
QY	415 TGGCAGGTGCATGCACTCAGTTTCTTGCTTCCACTTGGGATTTCTTTCCACAGGKC 474

	B6614082	995 bp	mRNA	linear	EST 18-APR-2002
DEFINITION	602641734P1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4772673 5' ,				
Locus					
ACCESSION	B6614082				
VERSION	B6614082.1 GI:13665453				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LNCMI643 row: C column: 10 High quality sequence stop: 668. Location/Qualifiers				
FEATURES	source				
	1..895				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone_image="IMAGE:4772673"				
	/clone_id="NIH_MGC_61"				
	/tissue_type="embryonal carcinoma"				
	/lab_host="DH10B (TI phage-resistant)"				
	/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:"				
	SfiI (ggcgccctgcgccc), Site_2: SfiI (ggccattatgcc)." 5'				
	Double-stranded cDNA was prepared from cell line RNA. 5'				
	and 3' adaptors were used in cloning as follows: 5'				
	adaptor sequence: 5'-CACGCCATTAAGGCGC-3' and 3' adaptor				
	sequence: 5'-ATTCTAGAGCGGAGGGCGGCAGCATG-df(30)BN-3'				
	(where B = A, C, or G and N = A, C, G, or T). Average				
	insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies				
	contained inserts by PCR. This library was enriched for				
	full-length clones and was constructed by Clontech				
	Laboratories (Palo Alto, CA). Note: this is a NIH-MGC				
	Library."				
BASE COUNT	226 a 203 c 215 g 251 t				
ORIGIN					
Query Match	78.8%; Score 558.4; DB 12; Length 895;				
Best Local Similarity	89.6%; Pred. NO. 1.6e-155;				
Matches 660; Conservative	1; Mismatches 8; Indels 68; Gaps 3;				

39 TCTTCCTCCGCTTGCCTGTGAGCTGAGCGGCTGTATGTGCGGCAATACATGTCAACC 98
 4 TCTTCCTCCGCTTGCCTGTGAGCTGAGCGGCTGTATGTGCGGCAATACATGTCAACC 63
 99 CCGCTGCCCGCATGTGCTGCCCGCCCGGAAGGCGACCGCTGGCGGATTTTCCTGCAT 158
 64 CCGCTGCCCGCATGTGCTGCCCGCCCGGAAGGCGACCGCTGGCGGATTTTCCTGCAT 123
 159 GGATTGGAGATGACTG----- 175
 124 GGATTGGAGATGACTGCGGACGAGATGGGACAGAGCCTTTGCAAGGTATCAGAGTTCACAT 183
 176 -----GCCGTGTAGGCGCTGTATACATTAATATGAGCGTGCCT 212
 184 ATCAATATATCTGCCCGCATGCGCTGTAGGCGCTGTATACATTAATATGAGCGTGCCT 243
 213 ATGCTTATGATGATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 272
 244 ATGCTTATGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 303
 273 ATTAACAGGAGAGAGAAATATATAAGCTTTGATGATGATGATGATGATGATGATGATGATGAT 332
 304 ATTAACAGGAGAGAGAAATATATAAGCTTTGATGATGATGATGATGATGATGATGATGATGAT 363
 333 CCTTCTACAGATATTTTGGAGGCTTTCTCAGGAGAGAGCTTTATCTTTATATAT 392
 364 CCTTCTACAGATATTTTGGAGGCTTTCTCAGGAGAGAGCTTTATCTTTATATAT 423
 393 GCCCTTACAGAGAGAGAACTGGAGGCTGTACCTGACCTGCTTCTGCTCCACTT 452
 424 GCCCTTACAGAGAGAGAACTGGAGGCTGTACCTGACCTGCTTCTGCTCCACTT 483
 453 CGGCTTCTTCCACAGAGGCTGTACCTGCTGCTTATAGATATTTCTATCTCCAG 512
 484 CGGCTTCTTCCACAGAGGCTGTACCTGCTGCTTATAGATATTTCTATCTCCAG 543
 513 TGCCACGAGGAGTTGTGACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
 544 TGCCACGAGGAGTTGTGACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
 573 CTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 632
 604 CTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
 633 AGTTCGTCTCAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
 664 AGTTCGTCTCAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 722
 692 AATTGATGACGCTACT 708
 723 AATTGATGACGCTACT 739
 RESULT 12
 B1550895 711 bp mRNA linear EST 05-SEP-2001
 LOCUS B1550895 603195310F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5274938 5',
 DEFINITION mRNA sequence.
 ACCESSION B1550895
 VERSION B1550895.1 GI:15438207
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 711)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@bncf.nih.gov
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1694 row: c column: 03
 High quality sequence stop: 708.
 Location/Qualifiers
 1. 711
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5274938"
 /clone_1ib="NIH_MGC_95"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /note="Organ: Brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTT-3',
 size-selected for average insert size 2.5 kb and
 normalized to 10^5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."
 BASE COUNT 179 a 158 c 178 g 196 t
 ORIGIN
 Query Match 78.6%; Score 557.6; DB 13; Length 711;
 Best Local Similarity 89.7%; Pred. No. 2.5e-155;
 Matches 636; Conservative 1; Mismatches 6; Indels 66; Gaps 1;
 47 CCGCTTGGCGTGTGAGCTGAGCGGCTGTATGTCGGCAATACATGTCACCCCGCTGCC 106
 3 CGGCTGCGCTGTGAGCTGAGCGGCTGTATGTCGGCAATACATGTCACCCCGCTGCC 62
 107 CGGCATCGTGCCTGCCCGCCCGGAAGGCCACCGCTGCGGATTTTCTCATGATGATGG 166
 63 CGGCATCGTGCCTGCCCGCCCGGAAGGCCACCGCTGCGGATTTTCTCATGATGATGG 122
 167 AGATGCTG----- 175
 123 AGATGCTGCGGACGAGATGGGACAGACCTTTGCGAGGTATCAGAGTTCACATATCAATA 182
 176 -----GCCGTGTAGGCGCTGTATACATTAATATGAGCGTGCCTG 220
 183 TATCTGCCCGCATGCGCTGTTAGGCTGTATATTAATATGAGCGTGCCTG 242
 221 ATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 280
 243 ATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 302
 281 GGCAGCAGAAATATATAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 340
 303 GGCAGCAGAAATATATAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 362
 341 CAGATATTTTGGAGGCTTTCTCAGGAGAGAGCTTTATCTTATATAGCGCTTAC 400
 363 CAGATATTTTGGAGGCTTTCTCAGGAGAGAGCTTTATCTTATATAGCGCTTAC 422
 401 CACACAGCAGAACTGGAGGCTGCTACCTGCTGCTTCTTCTCCACTTCCGAGNTTC 460
 423 CACACAGCAGAACTGGAGGCTGCTACCTGCTGCTTCTTCTCCACTTCCGAGNTTC 482
 461 CTTTCCACAGGKCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 520
 483 CTTTCCACAGGKCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
 521 GGATTGTACCTTTGGGCTTCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 580
 543 GGATTGTACCTTTGGGCTTCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
 581 ATTGTGAATCCAGCCATGTGACCTTTAAACCTATGAAGGTATGATGATGATGATGATGATGAT 640

contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

BASE COUNT 178 a 157 c 173 g 201 t

ORIGIN

Query Match 76.3%; Score 540.8; DB 12; Length 709;
Best Local Similarity 89.1%; Pred. No. 2.6e-150;
Matches 632; Conservative 1; Mismatches 9; Indels 67; Gaps 2;

49 GCTTCCGCTGTAGCTGAGGGGCTTATGTGCGCAATATGCAACCCCGTCCCG 108
1 GCTTCCGCTGTAGCTGAGGGGCTTATGTGCGCAATATGCAACCCCGTCCCG 60
109 CCATGCTGCGCGCCCGCGGAAAGCCACCGCTGCGGATTTCTCGATGATTTGGAG 168
61 CCATGCTGCGCGCCCGCGGAAAGCCACCGCTGCGGATTTCTCGATGATTTGGAG 120
169 ATACTGG----- 175
121 ATACTGGCAGAGATGGCAGAGCCTTGCAGGATCAGAAGTTCAATTCATAATATA 180
176 -----GCCTTTAGCCTGTTACATTAAATATGACGCGGCTATGCTTCAT 222
181 TCTGCCCGCATGCGCTGTAGCCTGTACATTAAATATGACGCTGTATGCTTCAT 240
223 GATTGATATTATTTGGGCTTACACAGATTCACAGAGGATGATTTGGATTTAAACAG 282
241 GATTGATATTATTTGGGCTTACACAGATTCACAGAGGATGATTTGGATTTAAACAG 300
283 CAGCAGAAATATATAAAGCTTTGATTCAGAGAGTGAAGATGCGATTCCTCTAACA 342
301 CAGCAGAAATATATAAAGCTTTGATTCAGAGAGTGAAGATGCGATTCCTCTAACA 360
343 GAATATTATTTGGAGGCTTTCTCAGAGAGAGCTTTATCTTATPACTGCCCTTACCA 402
361 GAATATTATTTGGAGGCTTTCTCAGAGAGAGCTTTATCTTATPACTGCCCTTACCA 420
403 CACAGCAAACTGGCAGGTGCTCACTGACATCTTCTGCTCCACTCCGCGGNTCCCT 462
421 CACAGCAAACTGGCAGGTGCTCACTGACATCTTCTGCTCCACTCCGCGGNTCCCT 480
463 TTCCACAGAGGCTATGCGGTGCTCTAATAGATATTCTTCTCAGTGCACAGGG 522
481 TTCCACAGAGGCTATGCGGTGCTCTAATAGATATTCTTCTCAGTGCACAGGG 540
523 ATTGTGACCTTTGGTCCCTGATGTTGCTTCTTACGCTGGAAAACTAAAAACAT 582
541 ATTGTGACCTTTGGTCCCTGATGTTGCTTCTTACGCTGGAAAACTAAAAACAT 600
583 TGTGTAATCCAGCAATGTGACTTTTAAACCTATGAAGGATGACACAGTTCGCTC 642
601 TGTGTAATCCAGCAATGTGACTTTTAAACCTATGAAGGATGACACAGTTCGCTC 660
643 AACAGGAATGATGATGTCAAGCA-TTCATTGATTAACCTCTTACCTC 690
661 AACAGGAATGATGATGTCAAGCAATTCATTGATTAACCTCTTACCTC 709

RESULT 15
LOCUS B1596291 725 bp mRNA linear EST 07-SEP-2001
DEFINITION 603243007F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5285569 5', mRNA sequence.
ACCESSION B1596291
VERSION B1596291.1 GI:15488702
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 725)

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL1721 row: n column: 02
High quality sequence stop: 721.

FEATURES
source
Location/Qualifiers
1..725
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5285569"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: Brain; Vector: pBluescript (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 165 a 177 c 194 g 188 t 1 others

Query Match 75.4%; Score 534.6; DB 13; Length 725;
Best Local Similarity 89.3%; Pred. No. 1.9e-148;
Matches 624; Conservative 1; Mismatches 7; Indels 67; Gaps 2;

1 GCCGCTGCACGCCCTTTGGGCGCGCGCGCGCTTCCTTCGCGCTGCG 60
27 GCCGCTGCACGCCCTTTGGGCGCGCGCGCGCTTCCTTCGCGCTGCG 86
61 AGCTGAGCGGTATGTGCGCAATACATGCAACCCCGCGCGCATGTCGCCG 120
87 AGCTGAGCGGTATGTGCGCAATACATGCAACCCCGCGCGCATGTCGCCG 146
121 CCGCCGGAAGGCGACCGCTGCGGATTTCTGTCATGATTTGGAGATCTGG 175
147 CCGCCGGAAGGCGACCGCTGCGGATTTCTGTCATGATTTGGAGATCTGG 206
176 ----- 175
207 GATGGCAGAAAGCCTTTGAGAGTATCAGAAATTCATATATATCCCGCATG 266
176 -GCCCTTAGGCGCTGTATACATTAAATATGACGTGCTATGCTTATGATTA 234
267 CGCGCTTAGGCGCTGTATACATTAAATATGACGTGCTATGCTTATGATTA 326
235 TTGGGCTTTCACAGATTCACAGAGGATGAATCTGGATTAACAGCAGAAATA 294
327 TTGGGCTTTCACAGATTCACAGAGGATGAATCTGGATTAACAGCAGAAATA 386
295 TAAACCTTTGATGATTCAGAGGATGAATCTGGATTAACAGCAGAAATA 354
387 TAAACCTTTGATGATTCAGAGGATGAATCTGGATTAACAGCAGAAATA 446
355 GAGGCTTTCTCAGAGGAGCTTTATCTTATATCTGCTTACACAGCAGAAAC 414
447 GAGGCTTTCTCAGAGGAGCTTTATCTTATATATCTGCTTACACAGCAGAAAC 506
415 TGGCAGGTTCACATGCACTTCTTCTGCTTCCACTTCGCGGATTCCTTCCACAGGKC 474

Db 507 TGGCAGGTGCTACCTGCACTGCTGCTGCTTCCACTTCGGGCTTCCTTCCACAGGCTC 566
Qy 475 CTATCGGTGGTGCCTAATAGAGATATTCTATTCCTCAGTGCACGGGATTGTGACCTT 534
|||
Db 567 CTATCGGTGGTGCCTAATAGAGATATTCTATTCCTCAGTGCACGGGATTGTGACCTT 626
Qy 535 TGGTCCCCCTGATGTTGGTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCCAG 594
|||
Db 627 TGGTCCCCCTGATG-TGGTCTCTTACGGTGGAAAACTAAAAACATTGGTGAATCCAA 685
Qy 595 CCATGTGACCTTTAAACCTATGAGGTATGATGCACA 633
|||
Db 686 GCATGTGACCTTTAAACCTATGAGGTATGATGCACA 724

Search completed: January 19, 2003, 03:13:56
Job time : 2238 secs